



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 09:46 PM UTC

PDB ID : 7BL6 / pdb_00007bl6
EMDB ID : EMD-12219
Title : 50S-ObgE-GMPPNP particle
Authors : Hilal, T.; Nikolay, R.; Schmidt, S.; Spahn, C.M.T.
Deposited on : 2021-01-18
Resolution : 4.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

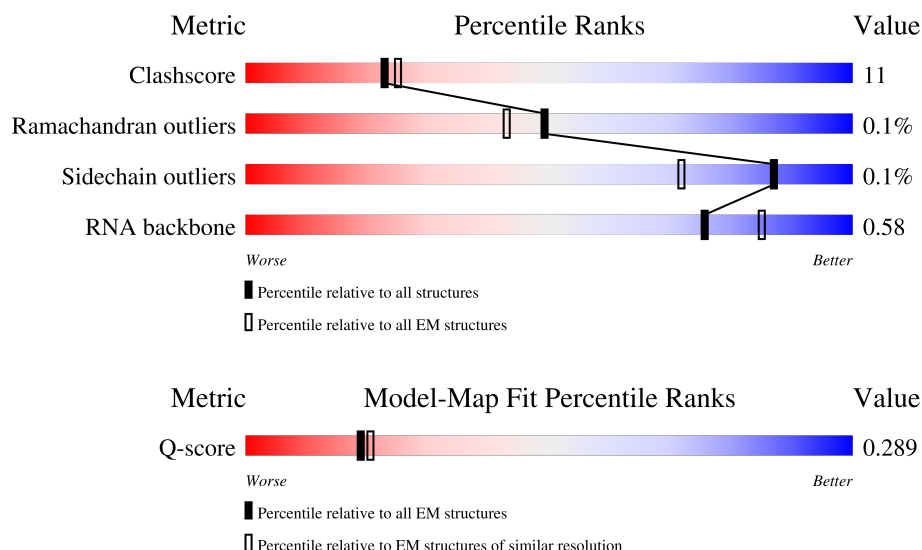
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



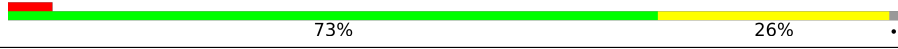
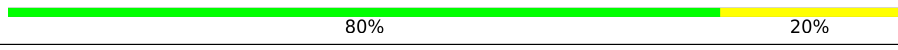
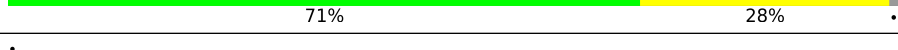
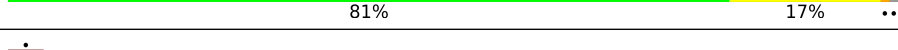
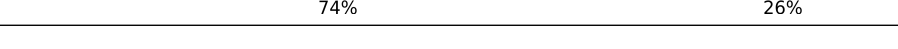
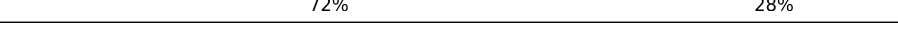
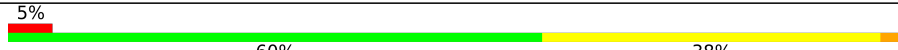
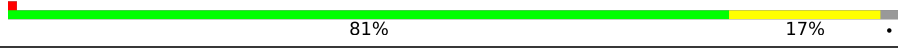
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	g	38	
2	C	273	
3	D	209	

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Mol	Chain	Length	Quality of chain
4	E	201	
5	F	179	
6	G	177	
7	J	142	
8	L	144	
9	N	120	
10	O	117	
11	Q	118	
12	R	103	
13	S	110	
14	T	100	
15	U	104	
16	V	94	
17	W	85	
18	X	78	
19	Y	63	
20	Z	59	
21	0	57	
22	1	55	
23	2	46	
24	K	123	
25	P	115	
26	M	136	
27	H	149	
28	d	70	

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Mol	Chain	Length	Quality of chain
29	A	2904	47% 47% 6%
30	B	119	48% 49%
31	9	390	7% 70% 17% 13%
32	3	65	68% 29%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 92769 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	193	Total	C	N	O	S	0	0
			1483	932	266	280	5		

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 8 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 10 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 11 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 12 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 13 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 14 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 15 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 16 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 17 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	W	76	Total	C	N	O	S	0	0
			577	357	117	102	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O		0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	113	Total	C	N	O	S	0	0
			911	571	178	161	1		

- Molecule 26 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 27 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 29 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 31 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

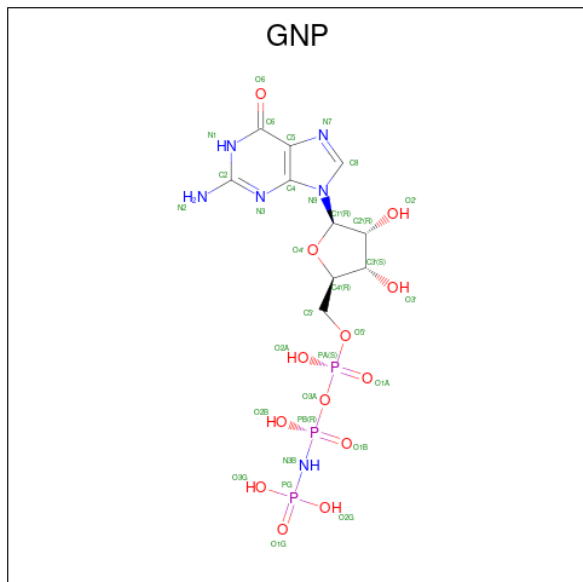
- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
33	g	1	Total	Zn	0
			1	1	
33	d	1	Total	Zn	0
			1	1	

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	A	1	Total	Mg	0
			1	1	
34	9	1	Total	Mg	0
			1	1	

- Molecule 35 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
35	9	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 36 is water.

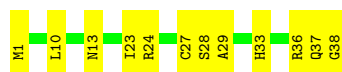
Mol	Chain	Residues	Atoms		AltConf
36	C	1	Total	O	0
			1	1	
36	F	1	Total	O	0
			1	1	
36	N	3	Total	O	0
			3	3	
36	S	1	Total	O	0
			1	1	
36	A	20	Total	O	0
			20	20	
36	B	1	Total	O	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

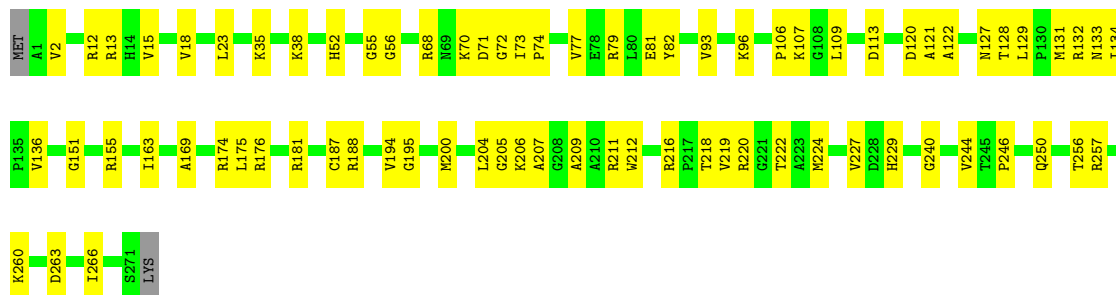
• Molecule 1: 50S ribosomal protein L36

Chain g: 



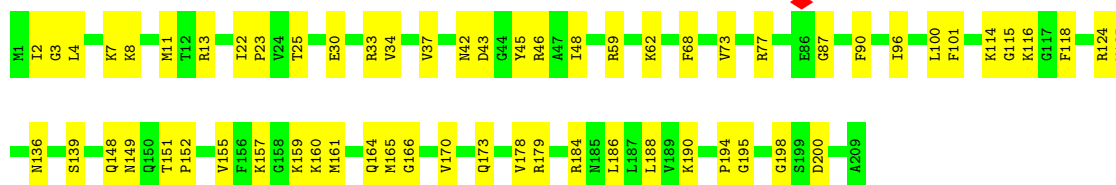
• Molecule 2: 50S ribosomal protein L2

Chain C: 



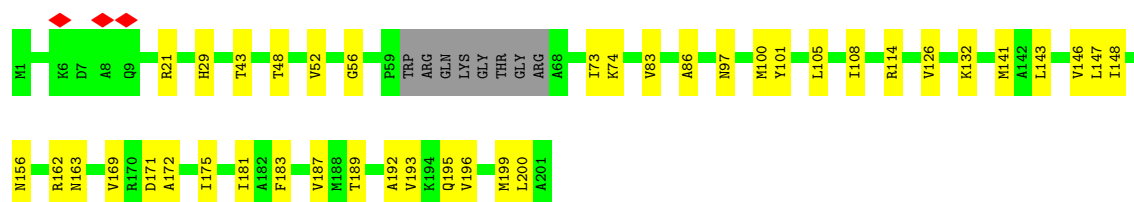
• Molecule 3: 50S ribosomal protein L3

Chain D: 

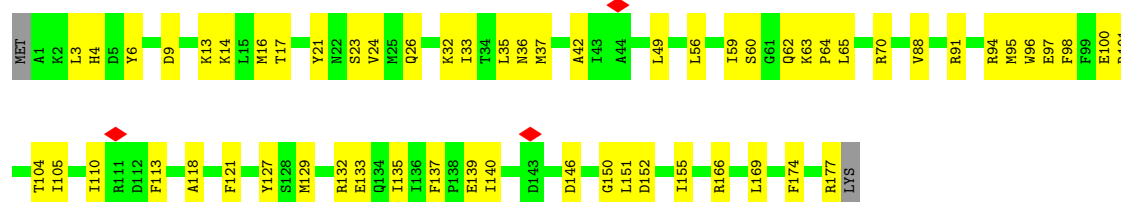


• Molecule 4: 50S ribosomal protein L4

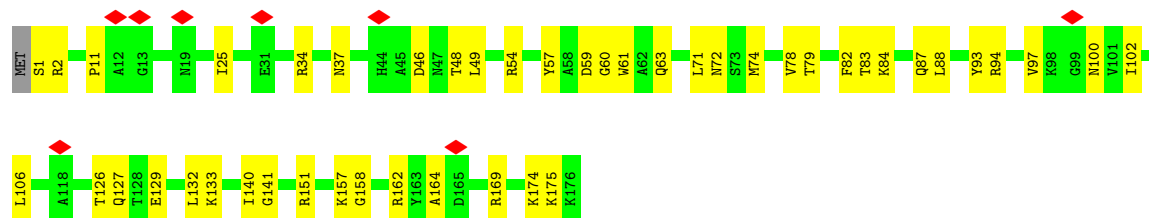
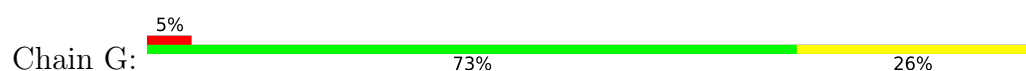
Chain E: 



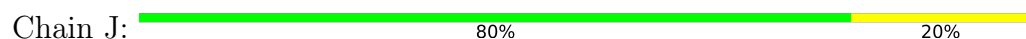
- Molecule 5: 50S ribosomal protein L5



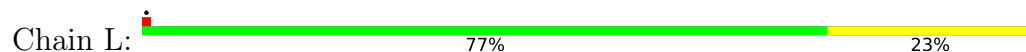
- Molecule 6: 50S ribosomal protein L6



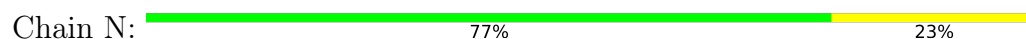
- Molecule 7: 50S ribosomal protein L13



- Molecule 8: 50S ribosomal protein L15

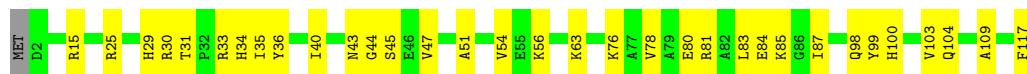


- Molecule 9: 50S ribosomal protein L17



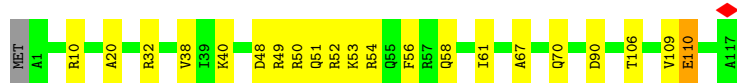
- Molecule 10: 50S ribosomal protein L18

Chain O:  71% 28%



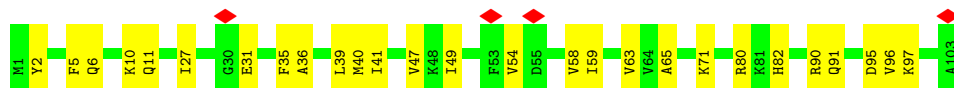
- Molecule 11: 50S ribosomal protein L20

Chain Q:  81% 17%



- Molecule 12: 50S ribosomal protein L21

Chain R:  74% 26%



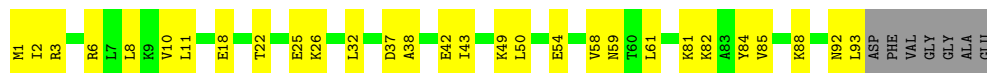
- Molecule 13: 50S ribosomal protein L22

Chain S:  72% 28%



- Molecule 14: 50S ribosomal protein L23

Chain T:  64% 29% 7%



- Molecule 15: 50S ribosomal protein L24

Chain U:  81% 17%



- Molecule 16: 50S ribosomal protein L25

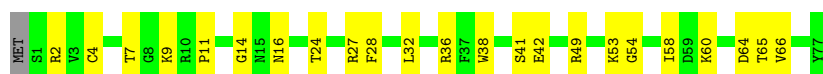
Chain V:  71% 29%



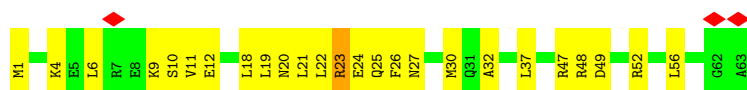
• Molecule 17: 50S ribosomal protein L27

Chain W: 

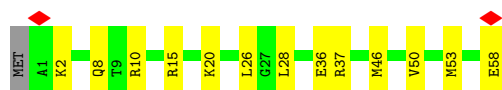
• Molecule 18: 50S ribosomal protein L28

Chain X: 

• Molecule 19: 50S ribosomal protein L29

Chain Y: 

• Molecule 20: 50S ribosomal protein L30

Chain Z: 

• Molecule 21: 50S ribosomal protein L32

Chain 0: 

• Molecule 22: 50S ribosomal protein L33

Chain 1: 

• Molecule 23: 50S ribosomal protein L34

Chain 2: 



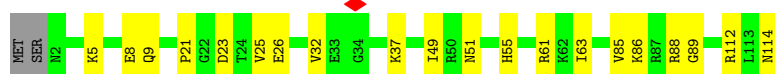
- Molecule 24: 50S ribosomal protein L14

Chain K: 70% 29%



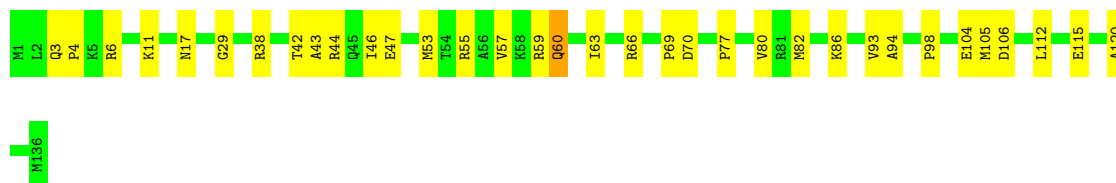
- Molecule 25: 50S ribosomal protein L19

Chain P: 81% 17%



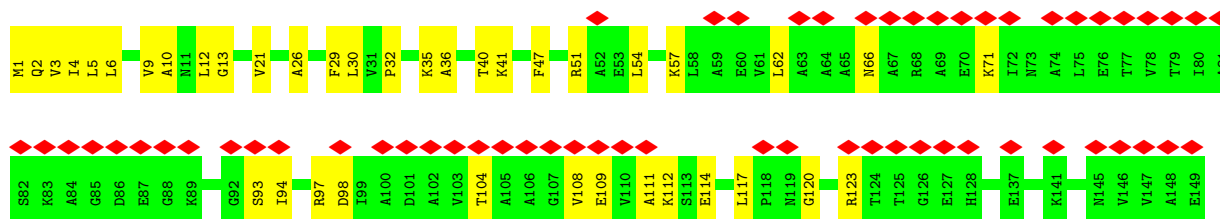
- Molecule 26: 50S ribosomal protein L16

Chain M: 75% 24%



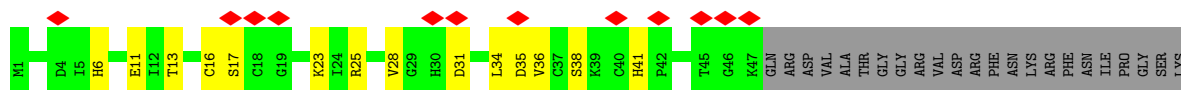
- Molecule 27: 50S ribosomal protein L9

Chain H: 40% 74% 26%



- Molecule 28: 50S ribosomal protein L31

Chain d: 17% 47% 20% 33%

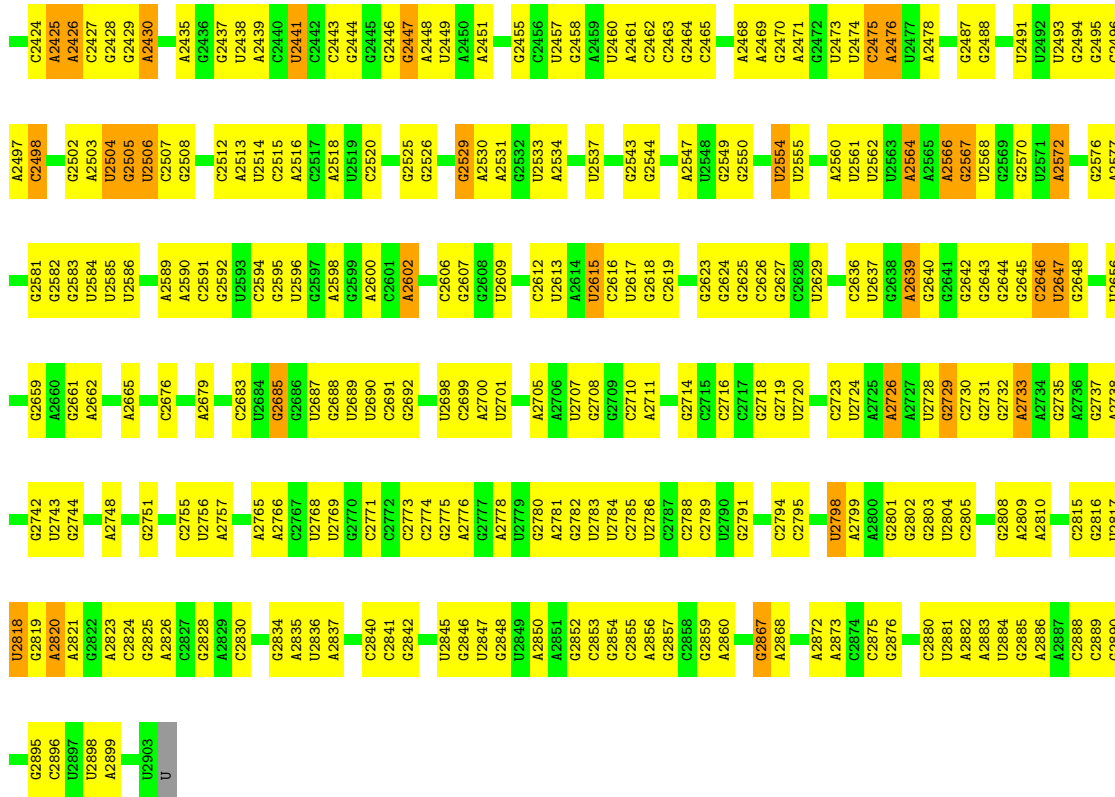


- Molecule 29: 23S ribosomal RNA

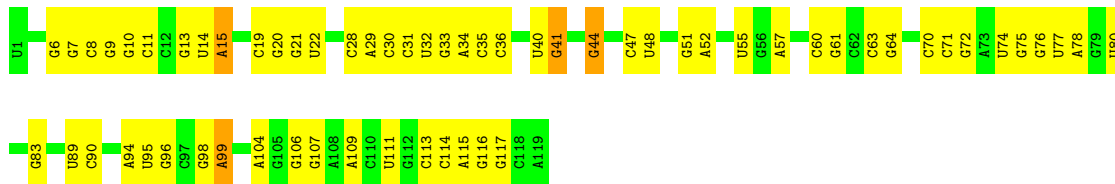
Chain A: 47% 47% 6%

U1132	C1045	U967	C	G805	C732	G648	U573	A805	C418	G329	U243	G159	C76	G1
A1133	A1046	C968	C	C806	A734	C649	A574	G505	U419	A330	A244	A160	G77	G2
C1136	A1047	C969	C	U807	A734	C650	A575	G506	C420	C331	G245	A161	U78	
G1137	A1048	U970	G	G808	A739	G651	G577	C509	G424	U339	C246	U162	C79	A5
A1138	G1056	A972	A892	G809	C740	A854	G578	C510		C340	G248	C163	A84	C7
G1139	A1057	A973	A896	U810	U741	A855	G579		A430	C341	C249	G168	A84	
C1140	U1058	G974	U811	U811	A742	A670	U580	A513	U431	C342		U169	U87	G9
U1141	G1059	A975	A900	C812	A743	A661	C581	A514	A432	U170	C253	U171	U87	
A1142	U1060	G976	G900	U813	U744	G662	A582	A515	C433	A95	C254	A95	C11	
	U1061	G977	C903	C814	G745	G663	C584	C517	U434	A172	A255	A173	U99	U12
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	U1066	A979	A905	C817	U747	A668	G585	U519	C436	U174	G259	U174	U100	A14
	A1067		U906	G818	G748	A669		U519	U437	G175		A176	A101	G15
C1153	G1068	C982	G907	A819	A749	A670	U589	G520	G438	A176	A265	G177	A101	C16
G1154	A1069	A983			A750	A671	U590	U521	A439	G177	G266	G177	A103	G17
A1155	A1070	C987	A910	A825	A751	C672	U591	A522	G442		C267	G178	A103	U18
A1156	G1071	A911	A911	U826	A752		U592	C523		A181			G106	A19
G1157	A1072	C912	C912	U827		A675	U593			A182	G271		G107	C20
	A1073	G989	U913	U828	U754		U594	A526	U451	A182	A272		G108	A21
	G1074		C915	A829			C595	A528	G452	C183	G273		C109	G22
		G993	C915	G830	C758	C678	U596	A529	A453	C184	A278		G110	G23
G1079	G1163	C994		G831	G759	C679	G597			G185			A111	G24
C1164	A1080	C995	A918	U832		C680	U598	A532	A457		A282		C116	U25
A1165	A1081	A996		A833	A764	G681	U598		G458	A191	G283		G117	G26
G1166		G997	C922	G834	C765	G682	G600	G536	U459	A196	G284		A118	A27
A1084	A1084	A1000		U839	U766	G683	G600	G536	A460	A197	U284		A119	G28
G1168	A1085	G923	C924	U839	U767	G684	C601	G537	G463	C198	G285		U120	U29
A1086	A1086	A1169	A925	A845	G768	A685	A602	A538	U464	A199	U286		A125	G30
G1087	G1087	C1005	G926	U846	U769	U886	A603	C539	U464	U200	G287		A126	C31
A1088	A1088	C1006	A927	U847	G770	C687		C540	G465	U201	U288		A127	C32
G1171	A1089	C1007		U848		U888	C611	G612	A466	U202	U290		A128	C33
U1173		A1008	U931	C848	U773	A689	A613	C542	G467	A203	U290		C128	
U1174	A1098	A1009	U932	A849	G774		A614	G543	G468		U296		C129	
A1175	G1099	U933	U933	U850	G775	C692	U615	U544	A472	U206	U296		G130	A38
G1176	C1100	U1012	U934	C851	C776	A693		U545		U207	G298		A131	G45
U1177	U1101	C1013	C935	U852	C777	A694	A621	U546	C475		G298		G46	
C1178	A1102	U1014	A936	G895	G778	G695		A547	A476	C386	A299		C47	
G1179	U1103	U1015	C937	G857	U779	G696	G625	G548	G476	C210	A300		G48	
U180	G1104	G1016	G938	G858	G780	G697	A626	G549	A477	C393	G301		G49	
	U1105		G939	G859	A781	C698	G626	C550	A478	G212	C302		U135	G51
	G1106	U1019	G940	U860	A782		A827	G551	A479	A213	G303		G136	
U1188	U1107		A941		A783	G711	G628	U552	A480	G214	U304		U137	G55
A1189	U1108	G1022		G864	G784	G712	G628	G553	G481	G215	U306		U138	A56
G1190	C1109			U870	G785	G713	G630	U554	A482	U397	U306		U139	
C1196	G1110	G1026	C946		C786	U714	A631	G555	A482	A401	G307		C140	C61
U1197	A1111	A1027	C948	C873	C787	A715	A632	U558	G487	A402	G308		G141	U62
G1198	G1112	A1028	A878	G874	A788		A633	G559	G488	U403	A309		A142	A83
U1199	U1113	U1033	C951		A789	A718	C634	G559	A491	U405	A311		A145	A84
G1202	C1114	G1034	C952	A877	A792	U719	C635		A492				C145	U85
U1203	G1115	U1035	C953	G874	A793	U720	C636	A563	G493				C147	
A1204	G1116		G954				C637	C564		G408	G319		U87	G68
A1205	C1123	G1038		G861	C796	U724	U639	G565	A497		A320		C151	C89
G1206	G1124	A1039	C961	G862	G797	G725	U639	U566	G498	G411	U321		A152	G70
A1126	C1207	G1040	G962	G883	G798	A727	U641	U567	U499	A412	A322		G232	A71
C1208	U1126	G1041	U963	U884	A772	G728	U641	U568	G500	C413	A324		A155	U72
		G1042	C964	U885	G799	G729	C645	G570		C414	A324		A156	A73
		C1043		A	A800	G729	C645	U571		C239			C157	U74
	U1130	C1043	C965		G801	A730	U646	A503	A504		G327		U158	C75
	A1131	C1043	C965		C847		A572							

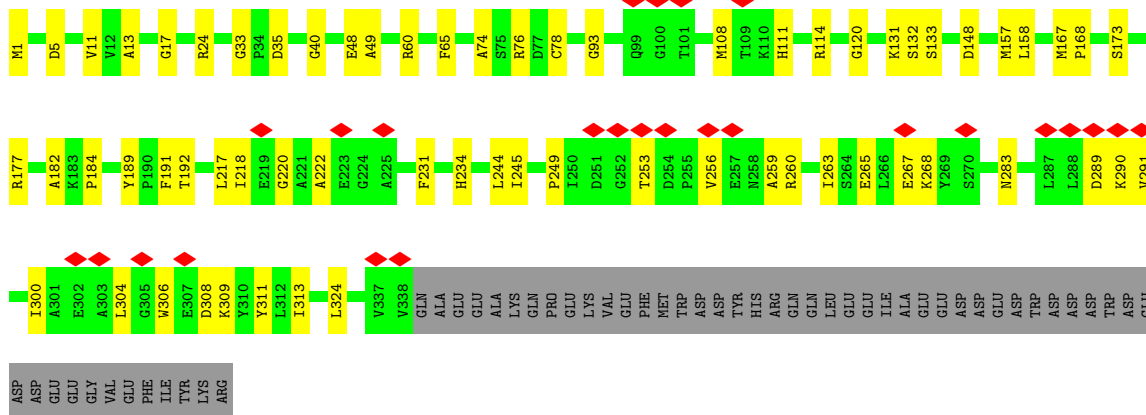
A2336	U2249	U2166	C2072	C2000	G1907	A1802	G1720	U1539	G1441	U1372	A1286	U1217
C2339	G2250	A2170	U2076	C2008	C1908	G1807	G1721	G1540	U1442	G1377	A1287	G1218
A2340	C2254	A2171	U2076	A2009	G1909	A1808	G1722	G1543	U1443	A1378	G1288	U1219
G2341	G2255	U2172	U2081	G2010	G1910	A1809	G1724	A1544	G1444	U1379	G1291	G1220
C2342	G2256	A2173	A2082	U2011	A1810	A1810	G1725	A1545	G1446	G1380	G1292	G1221
U2343	U2257	C2178	U2086	G2012	A1913	G1811	C1726	A1548	C1447	G1381	G1293	U222
G2344	C2258	C2178	G2087	A2013	C1914	U1812	C1727	A1549	G1452	G1382	G1294	G1223
U2345	U2262	U2182	A2088	U2017	U1915	G1813	C1728	C1550	A1453	G1383	U1294	U1224
A2346	C2263	A2183	C2089	G2018	U1918	C1816	U1729	C1551	G1458	C1384	C1295	U1225
C2347	U2264	A2090	A2090	A2019	A1918	G1817	C1730	A1551	U1458	C1386	A1296	A1226
C2350	U2265	U2187	C2093	A2020	A1919	U1818	G1731	G1555	U1458	C1387	G1298	C1229
G2357	A2266	C2093	C2093	C2021	U1923	G1732	G1732	C1556	G1461	A1388	G1299	A1230
G2360	A2267	C2096	C2096	U2022	U1923	G1733	G1733	C1557	C1461	G1389	G1300	U1231
G2361	G2271	C2096	C2096	C2023	U1926	G1734	G1734	C1558	C1462	U1390	A1301	G1232
C2362	U2099	U2099	U2099	G2024	U1926	U1736	A1736	G1559	C1463	U1391	A1302	U1233
G2363	G2100	C2025	C2025	C2025	A1927	G1737	G1737	G1560	C1464	A1392	G1293	U1234
A2364	U2026	U2026	U2026	U2026	U1825	G1738	G1738	C1561	C1465	A1393	G1294	U1235
G2365	G2027	G2027	G2102	G2027	G1830	A1739	G1739	U1562	U1466	U1394	G1309	G1236
C2368	A2198	A2199	G2101	U2028	U1931	U1827	U1742	U1563	U1467	U1396	G1310	G1237
A2369	G2200	G2201	G2102	G2029	U1936	G1828	U1743	U1564	U1468	U1397	G1238	G1238
G2370	A2287	G2201	U2109	A2030	A1936	G1829	U1744	C1565	U1476	C1398	C1314	U1242
C2371	U2288	U2202	G2110	A2031	A1937	C1830	A1744	A1566	U1477	C1399	G1315	U1243
G2372	G2289	G2203	U2111	G2032	G1941	G1831	A1745	A1567	G1476	U1400	C1320	C1243
C2373	G2290	G2204	G2112	A2033	C1942	C1832	G1748	A1568	A1477	G1401	A1321	A1244
A2377	C2285	A2199	G2116	U2034	G1942	C1833	C1748	A1569	G1482	C1404	G1250	G1250
C2383	G2286	G2200	A2117	G2035	C1943	U1834	A1668	A1570	G1501	U1406	C1261	C1261
A2384	A2287	G2201	U2118	C2036	U1944	G1835	A1669	A1571	G1502	U1405	A1262	G1252
C2385	G2288	U2202	G2120	A2037	U1944	C1836	C1670	A1572	G1503	G1407	U1263	G1253
A2386	A2289	G2203	U2119	G2038	C1947	G1837	U1671	U1578	G1490	U1408	A1254	A1254
G2389	G2290	G2204	G2121	U2039	G1948	G1838	G1753	C1582	U1493	U1409	U1256	U1256
U2390	C2304	G2216	G2122	G2040	G1954	G1674	A1754	U1583	G1495	G1410	G1257	G1257
G2391	U2305	G2217	U2122	C2043	U1955	C1675	A1676	C1585	U1497	U1412	U1258	U1258
C2394	G2308	G2220	A2126	C2044	U1956	A1676	A1757	C1585	G1498	A1413	G1259	G1259
U2402	A2311	G2221	G2127	C2045	C1962	A1848	A1762	U1589	G1501	G1416	A1260	A1260
C2403	U2312	A2225	G2128	G2046	C1963	G1849	G1763	A1590	G1502	G1417	C1261	C1261
U2404	C2313	C2226	C2129	C2047	U1965	G1850	C1764	A1591	G1503	G1418	A1262	A1262
G2405	A2314	A2227	U2131	G2048	C1966	U1851	G1682	C1592	G1346	G1419	U1263	U1263
A2406	G2315	G2228	U2132	A2052	C1967	U1852	C1771	A1593	A1504	A1419	A1264	A1264
U2402	G2316	U2229	G2133	C2052	G1968	A1858	A1772	U1594	A1515	A1420	A1265	A1265
C2403	A2317	G2230	A2134	C2055	A1969	U1859	A1773	C1597	A1516	G1424	G1266	G1266
U2404	G2318	U2231	G2135	G2056	U1971	G1862	U1779	A1597	G1517	G1425	U1267	U1267
G2405	U2320	C2232	G2136	A2058	G1972	C1863	A1780	A1598	C1518	C1428	A1268	A1268
A2406	A2322	G2234	U2139	A2059	U1977	U1864	A1784	G1601	G1519	G1429	A1269	A1269
G2410	G2325	G2238	G2140	G2061	A1977	C1869	C1788	U1603	U1520	G1430	G1271	G1271
A2411	C2326	G2239	C2145	A2062	A1987	G1869	A1789	A1607	A1522	A1431	A1272	A1272
A2412	A2327	U2240	C2146	C2063	G1988	C1870	A1789	A1608	G1523	G1432	A1275	A1275
G2413	A2328	A2241	C2147	C2064	U1991	A1871	A1791	C1607	G1524	A1433	G1276	G1276
G2414	U2329	G2242	G2148	C2065	U1991	C1874	A1791	A1608	G1525	A1434	C1362	C1362
G2415	G2330	U2244	G2148	G2066	G1992	G1875	U1796	G1611	A1528	G1435	C1363	C1363
C2416	G2330	U2245	G2157	U2068	U1993	G1875	U1797	A1614	G1533	G1436	G1279	G1279
G2417	A2333	G2246	A2153	G2069	C1996	U1880	U1798	C1615	U1534	C1437	A1365	A1365
A2418	U2334	A2247	C2164	C2070	C1997	C1881	U1799	G1615	U1534	U1438	G1281	G1281
U2419	A2335	C2248	C2165	A2071	C1999	A1890	A1801	G1620	A1535	A1439	U1282	U1282



• Molecule 30: 5S ribosomal RNA



• Molecule 31: GTPase ObgE/CgtA



● Molecule 32: 50S ribosomal protein L35

Chain 3:  68% 29% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	45746	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.195	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.034	Depositor
Map value standard deviation	0.170	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	417.6, 417.6, 417.6	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.74, 1.74, 1.74	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	g	0.12	0/303	0.33	0/397
2	C	0.10	0/2121	0.31	0/2852
3	D	0.09	0/1586	0.28	0/2134
4	E	0.10	0/1499	0.28	0/2016
5	F	0.12	0/1434	0.36	0/1926
6	G	0.10	0/1343	0.29	0/1816
7	J	0.10	0/1152	0.29	0/1551
8	L	0.10	0/1062	0.34	0/1413
9	N	0.12	0/974	0.34	0/1301
10	O	0.13	0/902	0.40	0/1209
11	Q	0.14	0/960	0.42	1/1278 (0.1%)
12	R	0.10	0/829	0.32	0/1107
13	S	0.10	0/864	0.29	0/1156
14	T	0.11	0/744	0.35	0/994
15	U	0.10	0/787	0.30	0/1051
16	V	0.12	0/766	0.39	0/1025
17	W	0.09	0/584	0.28	0/772
18	X	0.09	0/635	0.28	0/848
19	Y	0.18	0/510	0.58	1/677 (0.1%)
20	Z	0.10	0/453	0.32	0/605
21	0	0.11	0/450	0.40	0/599
22	1	0.09	0/416	0.26	0/554
23	2	0.10	0/380	0.34	0/498
24	K	0.10	0/947	0.31	0/1268
25	P	0.10	0/923	0.29	0/1234
26	M	0.10	0/1093	0.33	0/1460
27	H	0.12	0/1121	0.39	0/1515
28	d	0.11	0/371	0.33	0/496
29	A	0.07	0/69659	0.18	0/108672
30	B	0.06	0/2847	0.15	0/4440
31	9	0.11	0/2626	0.32	0/3542
32	3	0.10	0/513	0.38	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.08	0/100854	0.23	2/151082 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Q	110	GLU	N-CA-CB	5.09	118.17	110.28
19	Y	23	ARG	CB-CG-CD	5.01	122.83	111.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	g	302	0	340	10	0
2	C	2082	0	2157	61	0
3	D	1565	0	1616	45	0
4	E	1483	0	1548	26	0
5	F	1410	0	1447	47	0
6	G	1323	0	1374	31	0
7	J	1129	0	1162	21	0
8	L	1053	0	1129	26	0
9	N	961	0	1000	22	0
10	O	892	0	923	23	0
11	Q	947	0	1022	17	0
12	R	816	0	839	19	0
13	S	857	0	922	21	0
14	T	738	0	807	23	0
15	U	779	0	834	15	0
16	V	753	0	780	21	0
17	W	577	0	594	12	0
18	X	625	0	655	16	0
19	Y	509	0	543	21	0
20	Z	449	0	491	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	0	444	0	461	12	0
22	1	409	0	440	12	0
23	2	377	0	418	11	0
24	K	938	0	1012	26	0
25	P	911	0	957	13	0
26	M	1074	0	1157	23	0
27	H	1110	0	1148	28	0
28	d	364	0	364	12	0
29	A	62195	0	31280	1125	0
30	B	2548	0	1292	55	0
31	9	2582	0	2606	45	0
32	3	504	0	574	16	0
33	d	1	0	0	0	0
33	g	1	0	0	0	0
34	9	1	0	0	0	0
34	A	1	0	0	0	0
35	9	32	0	13	2	0
36	A	20	0	0	0	0
36	B	1	0	0	0	0
36	C	1	0	0	0	0
36	F	1	0	0	0	0
36	N	3	0	0	0	0
36	S	1	0	0	0	0
All	All	92769	0	61905	1672	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (1672) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1433:A:N6	29:A:1560:G:H1	1.63	0.96
29:A:408:G:H1	29:A:419:U:H3	1.08	0.95
29:A:2102:G:H1	29:A:2187:U:H3	1.17	0.92
29:A:2475:C:H42	29:A:2529:G:H22	1.13	0.91
29:A:377:G:H1	29:A:397:U:H3	0.93	0.90
29:A:1433:A:H61	29:A:1560:G:H1	0.90	0.89
29:A:2204:G:H1	29:A:2220:U:H3	1.20	0.89
29:A:2475:C:H42	29:A:2529:G:N2	1.71	0.88
31:9:157:MET:HE3	31:9:158:LEU:H	1.41	0.84
29:A:78:U:H3	29:A:108:G:H1	1.24	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:37:GLN:HE21	29:A:1125:G:H4'	1.40	0.84
29:A:285:G:H1	29:A:355:U:H3	1.23	0.84
29:A:1390:U:H3	29:A:1395:A:H62	1.25	0.83
29:A:1171:G:N1	29:A:1178:C:N3	2.26	0.83
29:A:639:U:H3	29:A:649:G:H1	1.27	0.83
29:A:2475:C:N4	29:A:2529:G:H22	1.79	0.80
4:E:100:MET:HE1	29:A:600:G:H1'	1.64	0.80
29:A:284:U:H3	29:A:356:G:H1	1.28	0.79
29:A:950:G:H1	29:A:967:U:H3	1.31	0.79
10:O:100:HIS:HA	10:O:104:GLN:HE22	1.48	0.78
14:T:25:GLU:HG3	14:T:26:LYS:HG2	1.68	0.75
29:A:1664:A:H61	29:A:1996:C:H42	1.33	0.75
23:2:12:ARG:HH22	29:A:464:U:H4'	1.52	0.74
29:A:2857:G:N2	29:A:2860:A:OP2	2.20	0.73
29:A:2898:U:H2'	29:A:2899:A:H8	1.52	0.73
3:D:46:ARG:HH22	3:D:87:GLY:H	1.36	0.73
31:9:244:LEU:HD22	31:9:283:ASN:HB2	1.70	0.73
29:A:171:U:H2'	29:A:172:A:H8	1.54	0.72
29:A:2093:G:N3	29:A:2198:A:N6	2.36	0.72
30:B:114:C:H2'	30:B:115:A:H8	1.54	0.72
31:9:5:ASP:O	31:9:60:ARG:NH1	2.22	0.72
18:X:32:LEU:HD12	18:X:49:ARG:HG2	1.72	0.71
5:F:129:MET:HA	29:A:2304:G:H4'	1.72	0.71
29:A:1105:U:H2'	29:A:1106:G:H8	1.55	0.71
29:A:1270:C:H5''	29:A:1271:G:H5'	1.71	0.71
29:A:488:G:H22	29:A:491:G:H5''	1.56	0.71
29:A:475:C:O2	29:A:479:A:N6	2.23	0.71
29:A:668:A:H2'	29:A:670:A:H62	1.55	0.71
29:A:1597:A:H5''	29:A:1598:A:H5'	1.72	0.70
29:A:160:A:N3	29:A:2208:C:O2'	2.23	0.70
5:F:3:LEU:HA	5:F:6:TYR:HB3	1.72	0.70
29:A:212:G:H2'	29:A:213:A:C8	2.26	0.70
31:9:217:LEU:HB3	31:9:231:PHE:HZ	1.56	0.70
26:M:77:PRO:HG2	26:M:80:VAL:HG21	1.73	0.70
29:A:463:G:N2	29:A:466:A:OP2	2.25	0.70
12:R:2:TYR:HE1	12:R:40:MET:HE1	1.58	0.69
5:F:36:ASN:HB3	5:F:152:ASP:HB2	1.74	0.69
29:A:1664:A:H61	29:A:1996:C:N4	1.91	0.69
29:A:1040:A:H61	29:A:1115:G:H1	1.38	0.69
29:A:1992:G:N2	29:A:1996:C:O2'	2.26	0.69
29:A:2120:G:H2'	29:A:2121:G:H8	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1528:A:OP2	29:A:1543:G:N2	2.26	0.69
29:A:371:A:H61	29:A:401:A:H3'	1.58	0.69
29:A:629:G:N3	29:A:639:U:O2'	2.27	0.68
29:A:937:C:H2'	29:A:938:G:H8	1.58	0.68
29:A:1834:U:H5''	29:A:1835:G:H5'	1.74	0.68
31:9:93:GLY:H	31:9:108:MET:HB2	1.58	0.68
29:A:2595:G:N2	29:A:2598:A:OP2	2.22	0.68
4:E:56:GLY:HA2	4:E:73:ILE:HG12	1.75	0.68
29:A:1363:C:O2'	29:A:1809:A:N3	2.28	0.67
4:E:163:ASN:ND2	29:A:320:A:N3	2.42	0.67
29:A:2233:U:H2'	29:A:2234:G:H8	1.59	0.67
29:A:2645:G:OP2	29:A:2645:G:N2	2.20	0.67
2:C:257:ARG:HB2	29:A:1798:U:H5''	1.76	0.67
22:1:24:LYS:NZ	22:1:25:ASN:O	2.27	0.67
24:K:121:GLU:HG2	24:K:122:VAL:H	1.59	0.67
19:Y:23:ARG:O	19:Y:27:ASN:ND2	2.24	0.67
29:A:177:G:OP2	29:A:177:G:N2	2.18	0.67
29:A:1664:A:N6	29:A:1996:C:H42	1.92	0.67
29:A:2258:C:O2'	29:A:2427:C:OP2	2.13	0.67
29:A:629:G:H1'	29:A:639:U:H1'	1.74	0.67
29:A:1057:A:N6	29:A:1087:G:OP2	2.28	0.67
29:A:1086:A:O2'	29:A:1087:G:N7	2.28	0.67
29:A:2229:U:H2'	29:A:2230:G:H8	1.58	0.67
29:A:2656:U:O2	29:A:2665:A:N7	2.27	0.66
2:C:35:LYS:HE3	29:A:1353:A:H4'	1.77	0.66
11:Q:106:THR:O	11:Q:109:VAL:HG12	1.95	0.66
29:A:2468:A:OP2	29:A:2476:A:N6	2.28	0.66
29:A:2497:A:N3	29:A:2498:C:N4	2.44	0.66
8:L:41:ARG:NH1	29:A:807:U:OP2	2.29	0.66
29:A:2581:G:N2	29:A:2581:G:OP2	2.29	0.66
29:A:373:U:H2'	29:A:374:A:H8	1.61	0.66
29:A:1171:G:N2	29:A:1178:C:O2	2.16	0.66
29:A:1779:U:OP2	29:A:1784:A:N6	2.29	0.66
18:X:58:ILE:HG22	18:X:66:VAL:HG11	1.77	0.65
5:F:9:ASP:O	5:F:13:LYS:NZ	2.28	0.65
29:A:2246:G:H2'	29:A:2247:A:H8	1.62	0.65
31:9:260:ARG:HE	31:9:304:LEU:HA	1.61	0.65
25:P:32:VAL:HG12	25:P:37:LYS:HG2	1.79	0.65
8:L:79:LEU:HD23	8:L:112:LEU:HA	1.79	0.65
29:A:1060:U:H4'	29:A:1061:U:H5'	1.77	0.65
29:A:1800:C:H42	29:A:1817:G:H22	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2514:U:H3	29:A:2570:G:H1	1.41	0.65
29:A:2515:C:H2'	29:A:2516:A:H8	1.62	0.65
4:E:132:LYS:NZ	29:A:320:A:OP2	2.29	0.65
12:R:63:VAL:HG22	12:R:96:VAL:HG12	1.79	0.65
29:A:26:G:H1'	29:A:515:A:H61	1.62	0.65
11:Q:48:ASP:HA	11:Q:51:GLN:HB2	1.79	0.65
29:A:2728:U:HO2'	29:A:2729:G:H8	1.45	0.65
29:A:177:G:H3'	29:A:178:G:H8	1.62	0.64
2:C:220:ARG:NH2	29:A:1788:C:OP1	2.31	0.64
29:A:213:A:H2'	29:A:214:G:C8	2.32	0.64
29:A:2816:G:N3	29:A:2883:A:O2'	2.29	0.64
1:g:1:MET:HE1	1:g:36:ARG:HB2	1.78	0.64
5:F:3:LEU:HD13	5:F:100:GLU:HG2	1.78	0.64
20:Z:2:LYS:NZ	20:Z:58:GLU:OE2	2.30	0.64
29:A:488:G:N1	29:A:491:G:OP2	2.31	0.64
17:W:68:LYS:NZ	30:B:11:C:OP1	2.24	0.64
22:1:5:ARG:NH2	29:A:2285:C:OP2	2.28	0.64
29:A:1696:G:N2	29:A:1977:A:O2'	2.28	0.64
4:E:29:HIS:HA	8:L:6:LEU:HD12	1.79	0.64
3:D:124:ARG:NH1	3:D:161:MET:O	2.31	0.64
29:A:222:A:H61	29:A:232:G:H1'	1.63	0.64
29:A:1351:C:O2'	29:A:1571:A:O2'	2.13	0.64
29:A:832:U:H2'	29:A:833:A:H8	1.62	0.64
29:A:848:C:H2'	29:A:849:A:H8	1.63	0.64
14:T:54:GLU:HG3	14:T:88:LYS:HD2	1.80	0.64
29:A:1668:A:N3	29:A:1670:C:N4	2.44	0.64
29:A:2059:A:H61	29:A:2503:A:H3'	1.63	0.64
29:A:1282:U:H3	29:A:1286:A:H62	1.46	0.64
29:A:99:U:H5''	29:A:100:U:H5'	1.78	0.63
29:A:324:A:OP2	29:A:1205:A:N6	2.32	0.63
3:D:62:LYS:HD3	29:A:2810:A:H4'	1.80	0.63
10:O:30:ARG:NH2	30:B:48:U:OP1	2.31	0.63
29:A:594:U:H3	29:A:663:G:H1	1.46	0.63
27:H:71:LYS:HZ3	27:H:108:VAL:HG21	1.63	0.63
29:A:1040:A:N6	29:A:1115:G:H1	1.96	0.63
22:1:25:ASN:OD1	22:1:27:ARG:NH1	2.32	0.63
26:M:55:ARG:HE	29:A:2469:A:H4'	1.64	0.63
29:A:514:A:N3	29:A:581:C:O2'	2.30	0.63
29:A:272:A:H2'	29:A:273:G:H8	1.63	0.63
29:A:1629:U:O4	29:A:1630:A:N6	2.31	0.63
29:A:1351:C:HO2'	29:A:1571:A:HO2'	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1724:G:O6	29:A:1737:G:N2	2.30	0.63
29:A:2730:C:H2'	29:A:2731:G:C8	2.34	0.62
6:G:106:LEU:HB3	6:G:151:ARG:HE	1.62	0.62
23:2:29:GLN:NE2	29:A:210:C:OP1	2.31	0.62
29:A:839:U:H3	29:A:939:G:H1	1.46	0.62
29:A:2163:A:OP1	29:A:2170:A:O2'	2.17	0.62
3:D:13:ARG:HA	3:D:23:PRO:HA	1.80	0.62
22:1:21:THR:HG21	29:A:2419:U:H4'	1.82	0.62
29:A:1926:U:O2'	29:A:1927:A:N7	2.30	0.62
16:V:4:ILE:HD12	16:V:42:LEU:HD11	1.81	0.62
29:A:571:U:O2'	29:A:573:U:OP2	2.17	0.62
29:A:1826:G:O2'	29:A:1971:U:OP2	2.16	0.62
12:R:10:LYS:NZ	29:A:994:C:O2	2.32	0.62
21:0:9:ARG:NH1	29:A:516:C:OP1	2.32	0.62
24:K:23:LYS:HB3	24:K:40:LYS:HB3	1.81	0.62
4:E:97:ASN:HB2	4:E:100:MET:HG2	1.81	0.62
31:9:309:LYS:NZ	31:9:311:TYR:OH	2.33	0.62
2:C:120:ASP:OD1	2:C:121:ALA:N	2.28	0.62
6:G:106:LEU:O	6:G:151:ARG:NH2	2.32	0.62
29:A:974:G:O2'	29:A:989:G:N2	2.33	0.62
29:A:1204:A:N6	29:A:1242:U:O4	2.32	0.62
29:A:1830:C:H2'	29:A:1831:G:H8	1.65	0.62
29:A:1999:C:O2	29:A:2687:U:O2'	2.17	0.62
5:F:132:ARG:HA	5:F:150:GLY:HA2	1.80	0.62
15:U:81:ARG:NH1	29:A:300:A:O5'	2.33	0.62
27:H:1:MET:N	27:H:21:VAL:O	2.32	0.62
29:A:371:A:N6	29:A:402:A:OP2	2.33	0.62
29:A:1123:C:H2'	29:A:1124:G:H8	1.64	0.62
29:A:2848:G:O2'	29:A:2867:G:N2	2.33	0.62
29:A:962:G:O2'	29:A:2250:G:N2	2.32	0.61
29:A:1353:A:OP2	29:A:1377:G:N1	2.32	0.61
29:A:1681:G:H21	29:A:1762:A:H3'	1.65	0.61
5:F:24:VAL:HG12	30:B:55:U:H4'	1.82	0.61
10:O:76:LYS:HB3	10:O:109:ALA:HB1	1.81	0.61
29:A:1288:G:OP2	29:A:1288:G:N2	2.33	0.61
20:Z:36:GLU:O	20:Z:37:ARG:NH1	2.33	0.61
29:A:787:C:H5''	29:A:788:A:H5'	1.82	0.61
3:D:42:ASN:ND2	3:D:43:ASP:OD2	2.33	0.61
29:A:1278:C:H2'	29:A:1279:G:C8	2.35	0.61
29:A:2081:U:H2'	29:A:2082:A:H8	1.66	0.61
1:g:23:ILE:HB	1:g:38:GLY:HA3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:131:MET:HE1	2:C:187:CYS:HB2	1.83	0.61
3:D:159:LYS:HB3	3:D:161:MET:HE1	1.83	0.61
29:A:818:G:N1	29:A:1188:U:OP2	2.28	0.61
31:9:11:VAL:HG12	31:9:65:PHE:HB2	1.81	0.61
19:Y:22:LEU:HD23	19:Y:23:ARG:HH11	1.65	0.61
31:9:157:MET:HE3	31:9:158:LEU:N	2.13	0.61
29:A:1278:C:H2'	29:A:1279:G:H8	1.65	0.61
29:A:1721:G:O2'	29:A:1739:A:N6	2.34	0.61
2:C:174:ARG:NH1	2:C:175:LEU:O	2.34	0.61
29:A:345:A:N3	29:A:347:A:N6	2.49	0.61
29:A:1165:A:H2'	29:A:1166:G:H8	1.66	0.61
30:B:28:C:H2'	30:B:29:A:H8	1.66	0.61
29:A:370:G:O2'	29:A:424:G:OP1	2.19	0.61
29:A:698:C:O2'	29:A:734:A:N6	2.23	0.61
29:A:1408:G:H1	29:A:1594:U:H3	1.48	0.61
29:A:1936:A:OP2	29:A:1962:C:N4	2.30	0.61
12:R:91:GLN:NE2	29:A:993:G:N3	2.47	0.60
17:W:37:ARG:NH2	29:A:2262:U:OP1	2.34	0.60
23:2:2:LYS:HE2	29:A:687:C:H5''	1.82	0.60
27:H:40:THR:O	27:H:41:LYS:HG3	2.01	0.60
29:A:482:A:O2'	29:A:497:A:N1	2.34	0.60
29:A:1443:U:H2'	29:A:1444:G:H8	1.67	0.60
29:A:1791:A:N6	29:A:1828:G:O2'	2.34	0.60
29:A:2735:G:H1	29:A:2769:U:H3	1.49	0.60
3:D:115:GLY:HA2	3:D:166:GLY:HA3	1.83	0.60
29:A:1463:C:H2'	29:A:1464:G:H8	1.67	0.60
2:C:70:LYS:HD2	2:C:73:ILE:HD12	1.83	0.60
2:C:260:LYS:HE2	29:A:2227:A:H5''	1.83	0.60
6:G:88:LEU:HD23	6:G:93:TYR:HB3	1.82	0.60
26:M:43:ALA:HA	26:M:46:ILE:HD12	1.82	0.60
29:A:2692:G:N3	29:A:2847:U:O2'	2.34	0.60
8:L:29:LYS:HE3	29:A:566:U:H5''	1.83	0.60
29:A:174:U:H2'	29:A:175:G:H8	1.67	0.60
29:A:184:C:H2'	29:A:185:G:H8	1.66	0.60
29:A:576:U:H2'	29:A:577:G:C8	2.37	0.60
2:C:23:LEU:HD21	2:C:82:TYR:HB2	1.83	0.60
31:9:13:ALA:HB3	31:9:148:ASP:H	1.67	0.60
2:C:122:ALA:O	2:C:127:ASN:ND2	2.32	0.59
2:C:244:VAL:HG12	2:C:250:GLN:HA	1.85	0.59
20:Z:8:GLN:HB2	20:Z:28:LEU:HD13	1.84	0.59
29:A:1992:G:O2'	29:A:1997:C:N4	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Y:9:LYS:N	19:Y:12:GLU:OE1	2.34	0.59
26:M:70:ASP:OD2	29:A:907:G:N2	2.35	0.59
27:H:111:ALA:HB3	27:H:114:GLU:HB2	1.85	0.59
29:A:23:G:H2'	29:A:24:G:H8	1.66	0.59
6:G:97:VAL:HG22	6:G:102:ILE:HG22	1.83	0.59
10:O:51:ALA:HB3	10:O:78:VAL:HG12	1.84	0.59
13:S:22:ASP:OD1	13:S:25:ARG:NH1	2.33	0.59
29:A:158:U:H3	29:A:168:G:H1	1.50	0.59
4:E:101:TYR:OH	4:E:175:ILE:O	2.21	0.59
5:F:37:MET:HA	5:F:37:MET:HE3	1.85	0.59
29:A:1056:G:H5''	29:A:1057:A:H5'	1.84	0.59
29:A:2591:C:N4	29:A:2592:G:O6	2.35	0.59
2:C:52:HIS:HA	2:C:216:ARG:HB2	1.83	0.59
22:I:25:ASN:ND2	29:A:2285:C:OP1	2.36	0.59
24:K:90:ASN:OD1	24:K:91:SER:N	2.36	0.59
29:A:1420:A:O2'	29:A:2211:A:N7	2.36	0.59
29:A:1432:G:H2'	29:A:1433:A:C8	2.37	0.59
29:A:2564:A:C2	29:A:2647:U:H4'	2.38	0.59
2:C:2:VAL:HG12	2:C:18:VAL:HG22	1.84	0.59
24:K:7:MET:HE3	24:K:8:LEU:H	1.68	0.59
29:A:1016:G:O6	29:A:1147:A:N6	2.36	0.59
29:A:272:A:H2'	29:A:273:G:C8	2.37	0.59
29:A:591:U:O4	29:A:592:A:N6	2.35	0.59
29:A:2776:A:O2'	29:A:2782:G:N7	2.32	0.59
5:F:70:ARG:NH2	29:A:2298:A:OP1	2.32	0.59
6:G:126:THR:HB	6:G:129:GLU:HB3	1.83	0.59
24:K:86:LEU:HB3	24:K:95:ILE:HD12	1.85	0.59
26:M:17:ASN:O	26:M:38:ARG:NH2	2.36	0.59
6:G:71:LEU:HA	6:G:74:MET:HG2	1.84	0.58
5:F:35:LEU:HD22	5:F:151:LEU:HD11	1.85	0.58
5:F:133:GLU:HG3	5:F:135:ILE:HG12	1.86	0.58
29:A:1754:A:N1	29:A:2716:C:O2'	2.35	0.58
29:A:2215:C:H2'	29:A:2216:G:H8	1.67	0.58
24:K:23:LYS:NZ	29:A:2561:U:O2	2.36	0.58
29:A:1812:U:H2'	29:A:1813:G:H8	1.68	0.58
2:C:220:ARG:NH1	29:A:1789:A:OP2	2.37	0.58
10:O:40:ILE:HG12	10:O:47:VAL:HG12	1.84	0.58
29:A:1969:A:H2'	29:A:1972:G:H21	1.68	0.58
29:A:2291:U:H1'	29:A:2374:C:H1'	1.86	0.58
29:A:1386:C:H2'	29:A:1387:A:H8	1.68	0.58
29:A:1390:U:H3	29:A:1395:A:N6	1.99	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1966:A:N6	31:9:133:SER:OG	2.37	0.58
2:C:68:ARG:NH1	2:C:128:THR:OG1	2.36	0.58
10:O:31:THR:OG1	10:O:34:HIS:O	2.15	0.58
25:P:88:ARG:NH1	25:P:114:ASN:OD1	2.36	0.58
29:A:926:G:H2'	29:A:927:A:C8	2.39	0.58
29:A:1681:G:OP2	29:A:1757:A:N6	2.34	0.58
29:A:1852:U:O2	29:A:1890:A:N6	2.32	0.58
24:K:64:ARG:HD3	24:K:102:PRO:HG2	1.86	0.58
27:H:104:THR:HG22	27:H:109:GLU:HA	1.86	0.58
29:A:6:A:H2'	29:A:7:G:H8	1.69	0.58
29:A:1469:A:OP2	29:A:1522:A:N6	2.36	0.58
14:T:37:ASP:OD1	14:T:38:ALA:N	2.31	0.58
25:P:5:LYS:HB3	25:P:9:GLN:HE22	1.68	0.58
1:g:28:SER:O	6:G:169:ARG:NH1	2.37	0.58
2:C:181:ARG:NH1	29:A:1800:C:OP2	2.36	0.58
26:M:6:ARG:NH2	29:A:870:U:OP1	2.37	0.58
29:A:1123:C:H2'	29:A:1124:G:C8	2.39	0.58
31:9:48:GLU:OE2	31:9:114:ARG:NH2	2.37	0.58
5:F:33:ILE:HG12	5:F:95:MET:HG2	1.86	0.57
14:T:2:ILE:HA	14:T:3:ARG:C	2.28	0.57
29:A:2245:U:H5''	29:A:2246:G:H5'	1.86	0.57
29:A:2788:C:O2'	29:A:2809:A:N3	2.32	0.57
2:C:206:LYS:NZ	29:A:729:G:OP2	2.35	0.57
14:T:18:GLU:OE2	29:A:1392:A:N6	2.37	0.57
18:X:9:LYS:NZ	29:A:397:U:OP2	2.36	0.57
29:A:1528:A:N6	29:A:1543:G:O2'	2.36	0.57
5:F:63:LYS:HD2	5:F:64:PRO:HD2	1.86	0.57
29:A:1682:G:OP2	29:A:1699:G:N2	2.37	0.57
29:A:2417:C:H2'	29:A:2418:A:C8	2.38	0.57
21:0:12:ARG:NH2	29:A:517:C:OP1	2.35	0.57
29:A:453:A:N3	29:A:457:A:O2'	2.38	0.57
29:A:741:U:H2'	29:A:742:A:H8	1.69	0.57
2:C:128:THR:HG22	2:C:188:ARG:HG2	1.87	0.57
15:U:81:ARG:HH12	29:A:300:A:H3'	1.70	0.57
8:L:96:LYS:HD3	8:L:103:ILE:HA	1.85	0.57
29:A:2246:G:H2'	29:A:2247:A:C8	2.39	0.57
29:A:968:C:H2'	29:A:969:G:C8	2.40	0.57
12:R:35:PHE:HB2	12:R:59:ILE:HB	1.87	0.57
24:K:70:ARG:NH1	29:A:2683:C:O2	2.31	0.57
29:A:633:A:O2'	29:A:2404:U:OP1	2.23	0.57
29:A:2730:C:H2'	29:A:2731:G:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2898:U:H2'	29:A:2899:A:C8	2.37	0.57
30:B:14:U:OP2	30:B:70:C:O2'	2.22	0.57
29:A:713:G:H21	29:A:718:A:H62	1.51	0.57
29:A:1386:C:H2'	29:A:1387:A:C8	2.39	0.57
29:A:1430:G:H1	29:A:1563:U:H3	1.53	0.57
29:A:2855:C:H2'	29:A:2856:A:H8	1.68	0.57
8:L:116:VAL:HG11	8:L:134:ALA:HB1	1.87	0.56
29:A:6:A:H2'	29:A:7:G:C8	2.40	0.56
29:A:1266:G:N2	29:A:2013:A:OP2	2.31	0.56
31:9:313:ILE:HD13	31:9:324:LEU:HD13	1.86	0.56
3:D:136:ASN:ND2	3:D:139:SER:O	2.38	0.56
29:A:1807:G:N2	29:A:1810:A:OP2	2.30	0.56
13:S:99:ARG:NH1	29:A:1262:A:OP1	2.38	0.56
20:Z:10:ARG:HB2	20:Z:53:MET:HB2	1.87	0.56
23:2:25:LYS:HA	23:2:28:ARG:HE	1.70	0.56
24:K:6:THR:HG23	29:A:1666:G:H4'	1.86	0.56
29:A:110:G:H2'	29:A:111:A:H8	1.71	0.56
29:A:377:G:N2	29:A:397:U:O2	2.31	0.56
29:A:948:C:H2'	29:A:949:G:H8	1.70	0.56
29:A:1358:G:N1	29:A:1372:U:OP2	2.31	0.56
29:A:2102:G:O6	29:A:2187:U:O4	2.23	0.56
29:A:2606:C:H2'	29:A:2607:G:C8	2.41	0.56
31:9:167:MET:HE1	31:9:245:ILE:HD13	1.87	0.56
5:F:139:GLU:HA	28:d:28:VAL:HG22	1.86	0.56
10:O:80:GLU:HA	10:O:83:LEU:HD12	1.87	0.56
17:W:36:GLN:HE22	17:W:41:PHE:HB2	1.70	0.56
29:A:541:A:N6	29:A:553:G:O6	2.38	0.56
29:A:2327:A:H2'	29:A:2328:A:C8	2.41	0.56
29:A:2443:C:H2'	29:A:2444:G:C8	2.41	0.56
29:A:2818:U:H3	29:A:2828:G:H1	1.54	0.56
2:C:77:VAL:HG12	2:C:93:VAL:HG12	1.88	0.56
29:A:1202:G:O6	29:A:1244:A:N6	2.38	0.56
29:A:2526:G:H1	29:A:2537:U:H3	1.52	0.56
29:A:577:G:O2'	29:A:1254:A:OP1	2.24	0.56
29:A:584:C:N4	29:A:585:G:O6	2.38	0.56
29:A:1196:C:H2'	29:A:1197:G:H8	1.71	0.56
29:A:1812:U:H2'	29:A:1813:G:C8	2.39	0.56
4:E:83:VAL:HB	4:E:86:ALA:HB2	1.87	0.56
14:T:8:LEU:HD12	14:T:50:LEU:HD21	1.87	0.56
26:M:105:MET:HA	26:M:105:MET:HE3	1.88	0.56
29:A:184:C:H2'	29:A:185:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:651:G:H5'	32:3:18:LYS:HG3	1.88	0.56
29:A:1807:G:H2'	29:A:1808:A:H5'	1.88	0.56
11:Q:50:ARG:NH2	29:A:993:G:OP2	2.38	0.56
29:A:935:C:H2'	29:A:936:A:H8	1.71	0.56
29:A:2743:U:OP2	29:A:2755:C:N4	2.39	0.56
4:E:126:VAL:O	4:E:156:ASN:ND2	2.39	0.56
10:O:63:LYS:NZ	30:B:51:G:OP1	2.36	0.56
29:A:5:A:H2'	29:A:6:A:H8	1.69	0.56
29:A:727:A:OP2	29:A:1431:A:O2'	2.23	0.56
29:A:780:G:N2	29:A:785:G:N7	2.53	0.56
29:A:2507:C:O3'	31:9:76:ARG:NH2	2.39	0.56
7:J:7:LYS:HG3	29:A:538:A:H4'	1.87	0.56
18:X:36:ARG:NH2	29:A:2199:A:OP1	2.35	0.56
29:A:2090:A:N6	29:A:2230:G:O6	2.39	0.56
7:J:13:ARG:NH2	7:J:49:ASP:OD2	2.38	0.55
19:Y:20:ASN:HA	19:Y:24:GLU:OE2	2.05	0.55
29:A:213:A:H2'	29:A:214:G:H8	1.72	0.55
29:A:1282:U:O4	29:A:1286:A:N7	2.39	0.55
16:V:7:GLU:HG2	16:V:41:GLU:HB3	1.88	0.55
17:W:63:VAL:HG12	17:W:78:ILE:HG12	1.89	0.55
29:A:1429:G:H2'	29:A:1430:G:H8	1.71	0.55
29:A:2345:G:H4'	29:A:2346:A:H3'	1.88	0.55
2:C:155:ARG:HD3	29:A:1818:U:H2'	1.89	0.55
3:D:179:ARG:HB2	3:D:188:LEU:HD12	1.88	0.55
26:M:11:LYS:HD3	26:M:86:LYS:HD3	1.88	0.55
29:A:1438:U:H2'	29:A:1439:A:H8	1.71	0.55
29:A:1709:U:O2'	29:A:2859:G:N3	2.34	0.55
22:1:25:ASN:ND2	22:1:28:THR:OG1	2.40	0.55
29:A:739:A:H1'	29:A:740:C:H5	1.70	0.55
29:A:1539:U:H2'	29:A:1540:G:H8	1.71	0.55
29:A:918:A:N3	30:B:80:U:O2'	2.39	0.55
29:A:1822:C:H2'	29:A:1823:G:H8	1.70	0.55
14:T:92:ASN:OD1	14:T:93:LEU:N	2.39	0.55
22:1:8:ILE:HD13	22:1:24:LYS:HD2	1.88	0.55
29:A:1518:C:H2'	29:A:1519:G:C8	2.41	0.55
31:9:49:ALA:O	31:9:111:HIS:ND1	2.39	0.55
3:D:2:ILE:HD13	3:D:48:ILE:HD11	1.89	0.55
4:E:189:THR:O	4:E:193:VAL:N	2.39	0.55
16:V:47:VAL:HA	16:V:50:MET:SD	2.46	0.55
29:A:434:U:O2	29:A:435:C:N4	2.33	0.55
29:A:1463:C:H2'	29:A:1464:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:98:GLN:NE2	30:B:47:C:O2'	2.37	0.55
29:A:987:C:O2'	29:A:1000:A:N3	2.37	0.55
29:A:1164:C:H2'	29:A:1165:A:H8	1.72	0.55
29:A:1501:G:H2'	29:A:1502:A:H8	1.71	0.55
29:A:1800:C:H42	29:A:1817:G:N2	2.05	0.55
29:A:2405:G:O2'	29:A:2411:A:N6	2.39	0.55
29:A:968:C:H2'	29:A:969:G:H8	1.71	0.55
29:A:1223:G:N2	29:A:1226:A:OP2	2.24	0.55
29:A:1461:C:H2'	29:A:1462:C:H6	1.72	0.55
29:A:1825:U:H2'	29:A:1826:G:H8	1.72	0.55
29:A:2192:U:H2'	29:A:2193:G:H8	1.71	0.55
29:A:2707:U:H2'	29:A:2708:G:H8	1.71	0.55
29:A:31:C:O2'	29:A:1238:G:OP1	2.24	0.54
29:A:739:A:N3	29:A:740:C:N4	2.55	0.54
29:A:2417:C:H2'	29:A:2418:A:H8	1.72	0.54
29:A:174:U:H2'	29:A:175:G:C8	2.41	0.54
29:A:2656:U:C2	29:A:2665:A:N7	2.74	0.54
15:U:81:ARG:NH1	29:A:301:G:OP2	2.38	0.54
29:A:244:A:OP2	32:3:7:ARG:NH2	2.40	0.54
29:A:552:U:H2'	29:A:553:G:H8	1.72	0.54
29:A:1400:U:H2'	29:A:1401:G:C8	2.42	0.54
29:A:1589:U:H2'	29:A:1590:A:C8	2.42	0.54
29:A:1688:U:O2'	29:A:1700:A:N7	2.31	0.54
29:A:1907:G:O6	29:A:1923:U:O2	2.24	0.54
5:F:104:THR:HG23	5:F:105:ILE:HG12	1.90	0.54
29:A:2623:G:H2'	29:A:2624:G:H8	1.73	0.54
29:A:2815:C:H2'	29:A:2816:G:H8	1.72	0.54
32:3:5:THR:HG22	32:3:62:PRO:HD2	1.89	0.54
1:g:10:LEU:HD12	1:g:33:HIS:HD2	1.72	0.54
2:C:15:VAL:HG22	2:C:205:GLY:HA3	1.88	0.54
4:E:43:THR:O	29:A:442:G:N2	2.40	0.54
5:F:127:TYR:HB3	5:F:155:ILE:HB	1.90	0.54
6:G:106:LEU:HD12	6:G:151:ARG:HG2	1.89	0.54
17:W:67:VAL:HG22	17:W:74:LYS:HG2	1.90	0.54
7:J:40:HIS:O	11:Q:70:GLN:NE2	2.38	0.54
9:N:103:ARG:NH1	29:A:1287:A:O4'	2.41	0.54
10:O:54:VAL:O	10:O:56:LYS:NZ	2.39	0.54
29:A:45:G:H5'	29:A:46:G:H5'	1.89	0.54
29:A:1433:A:H2'	29:A:1434:A:H8	1.73	0.54
29:A:2070:A:H2'	29:A:2071:A:H8	1.73	0.54
2:C:132:ARG:HH22	27:H:93:SER:HB3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:2:ARG:HD2	29:A:1653:G:H5''	1.90	0.54
29:A:1791:A:OP2	29:A:1828:G:N2	2.40	0.54
30:B:13:G:O2'	30:B:15:A:OP2	2.23	0.54
15:U:3:LYS:O	15:U:93:ARG:NH2	2.40	0.54
15:U:81:ARG:HG3	15:U:96:LYS:HD3	1.89	0.54
27:H:29:PHE:O	27:H:35:LYS:NZ	2.40	0.54
29:A:698:C:HO2'	29:A:734:A:H61	1.52	0.54
29:A:2320:U:O2'	29:A:2322:A:N6	2.41	0.54
3:D:116:LYS:NZ	29:A:2724:U:OP1	2.37	0.54
9:N:12:ARG:O	9:N:17:ARG:NH2	2.41	0.54
21:O:29:VAL:O	29:A:2885:G:N1	2.35	0.54
26:M:69:PRO:HA	26:M:94:ALA:HB2	1.90	0.54
29:A:932:U:O2'	29:A:934:U:O4	2.25	0.54
29:A:937:C:H2'	29:A:938:G:C8	2.42	0.54
23:2:39:ARG:NH2	29:A:468:G:O6	2.35	0.54
29:A:2047:C:H2'	29:A:2048:G:H8	1.72	0.54
30:B:114:C:H2'	30:B:115:A:C8	2.39	0.54
5:F:37:MET:HG2	5:F:56:LEU:HD11	1.89	0.53
29:A:2549:G:H2'	29:A:2550:G:H8	1.73	0.53
29:A:2818:U:H2'	29:A:2819:G:C8	2.43	0.53
3:D:148:GLN:O	29:A:2052:A:H4'	2.08	0.53
11:Q:40:LYS:HE3	29:A:563:A:H4'	1.88	0.53
13:S:17:VAL:HG11	13:S:103:ILE:HG12	1.89	0.53
22:1:36:LYS:HG2	22:1:47:ILE:HD13	1.91	0.53
7:J:102:GLU:HB2	7:J:119:PHE:HE2	1.73	0.53
8:L:30:THR:OG1	29:A:1190:G:OP1	2.26	0.53
15:U:67:SER:OG	29:A:327:G:N2	2.41	0.53
29:A:2070:A:H2'	29:A:2071:A:C8	2.43	0.53
4:E:171:ASP:OD2	4:E:172:ALA:N	2.39	0.53
6:G:46:ASP:O	6:G:48:THR:N	2.38	0.53
15:U:96:LYS:NZ	29:A:299:A:OP1	2.40	0.53
21:O:54:ILE:HG23	21:O:56:LYS:H	1.73	0.53
29:A:742:A:H2'	29:A:743:A:H8	1.74	0.53
7:J:3:THR:OG1	29:A:995:C:O2	2.26	0.53
30:B:72:G:H21	30:B:104:A:H62	1.56	0.53
1:g:1:MET:N	29:A:2526:G:N3	2.57	0.53
5:F:42:ALA:HB1	5:F:49:LEU:HD21	1.90	0.53
29:A:873:C:N4	29:A:874:G:O6	2.42	0.53
29:A:2328:A:H2'	29:A:2329:U:C6	2.44	0.53
3:D:37:VAL:HG22	3:D:48:ILE:HG22	1.91	0.53
7:J:17:VAL:HG22	7:J:55:ILE:HB	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:V:32:GLY:O	16:V:93:ARG:NH2	2.36	0.53
26:M:63:ILE:HG12	26:M:105:MET:HE1	1.90	0.53
29:A:574:A:N6	29:A:2034:U:OP1	2.41	0.53
29:A:742:A:H2'	29:A:743:A:C8	2.44	0.53
29:A:1649:G:O6	29:A:2009:A:N6	2.42	0.53
29:A:2059:A:N6	29:A:2504:U:OP2	2.42	0.53
3:D:151:THR:OG1	29:A:2032:G:N2	2.40	0.53
17:W:38:GLY:HA2	29:A:2330:G:H21	1.74	0.53
27:H:6:LEU:HD13	27:H:36:ALA:HA	1.91	0.53
29:A:222:A:N6	29:A:232:G:H1'	2.24	0.53
29:A:711:G:H1	29:A:720:U:H3	1.57	0.53
29:A:741:U:H2'	29:A:742:A:C8	2.44	0.53
29:A:1161:C:H2'	29:A:1162:G:H8	1.74	0.53
29:A:1170:C:N4	29:A:1171:G:O6	2.42	0.53
29:A:2447:G:H1	29:A:2451:A:H62	1.55	0.53
29:A:2687:U:H2'	29:A:2688:G:O4'	2.09	0.53
16:V:30:ILE:HD13	16:V:72:VAL:HG11	1.89	0.53
27:H:1:MET:SD	27:H:2:GLN:N	2.82	0.53
29:A:1281:G:H2'	29:A:1282:U:C6	2.44	0.53
29:A:2313:C:H2'	29:A:2314:A:H8	1.73	0.53
30:B:28:C:H2'	30:B:29:A:C8	2.44	0.53
6:G:1:SER:HA	6:G:61:TRP:HB3	1.91	0.53
9:N:114:GLU:HB2	9:N:118:ARG:HD2	1.91	0.53
29:A:796:C:H2'	29:A:797:G:C8	2.44	0.53
29:A:1171:G:O6	29:A:1178:C:N4	2.35	0.53
29:A:2192:U:H2'	29:A:2193:G:C8	2.45	0.53
6:G:158:GLY:O	6:G:162:ARG:NH1	2.41	0.52
13:S:83:LYS:HD2	13:S:95:ARG:HD2	1.91	0.52
13:S:55:ILE:HG23	13:S:66:ILE:HD11	1.92	0.52
25:P:25:VAL:HG22	25:P:85:VAL:HG22	1.91	0.52
29:A:1315:C:O2'	29:A:1392:A:N3	2.38	0.52
29:A:2339:C:H2'	29:A:2340:A:C8	2.44	0.52
29:A:696:G:H1	29:A:766:U:H3	1.57	0.52
29:A:2250:G:O2'	29:A:2496:C:OP1	2.27	0.52
1:g:27:CYS:HB2	1:g:33:HIS:HB2	1.90	0.52
3:D:34:VAL:HG23	3:D:96:ILE:HD11	1.91	0.52
4:E:162:ARG:NE	29:A:322:A:OP1	2.42	0.52
29:A:631:A:N3	29:A:2415:G:O2'	2.34	0.52
29:A:1048:A:H1'	29:A:1112:G:N2	2.25	0.52
29:A:1310:G:O2'	29:A:1611:C:OP1	2.27	0.52
29:A:2039:U:H2'	29:A:2040:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2443:C:H2'	29:A:2444:G:H8	1.74	0.52
32:3:51:LYS:HA	32:3:54:LEU:HD23	1.91	0.52
6:G:82:PHE:HB3	6:G:140:ILE:HD13	1.92	0.52
23:2:9:VAL:HG23	29:A:1309:G:H5''	1.90	0.52
29:A:935:C:H2'	29:A:936:A:C8	2.44	0.52
10:O:15:ARG:HH21	30:B:8:C:H5''	1.74	0.52
29:A:373:U:H2'	29:A:374:A:C8	2.42	0.52
29:A:645:C:H2'	29:A:647:G:C8	2.45	0.52
29:A:1013:C:H2'	29:A:1014:A:H8	1.74	0.52
29:A:2028:U:H3	29:A:2033:A:H62	1.57	0.52
29:A:2474:U:H5''	29:A:2475:C:H5	1.74	0.52
5:F:23:SER:OG	30:B:55:U:O2'	2.22	0.52
29:A:20:C:H2'	29:A:21:A:C8	2.44	0.52
29:A:305:C:H2'	29:A:306:U:C6	2.44	0.52
29:A:1161:C:H2'	29:A:1162:G:C8	2.43	0.52
29:A:1176:U:H2'	29:A:1177:G:C8	2.45	0.52
29:A:1380:G:H1'	29:A:1569:A:H61	1.74	0.52
29:A:1681:G:N2	29:A:1763:G:OP2	2.41	0.52
29:A:1800:C:N4	29:A:1817:G:H22	2.07	0.52
29:A:2659:G:H4'	31:9:1:MET:HE1	1.91	0.52
29:A:2728:U:O2'	29:A:2729:G:H8	1.91	0.52
31:9:177:ARG:HH11	31:9:182:ALA:H	1.56	0.52
29:A:145:C:H2'	29:A:146:A:H8	1.75	0.52
29:A:2637:U:H3	29:A:2776:A:H62	1.57	0.52
10:O:33:ARG:HG3	10:O:34:HIS:ND1	2.25	0.52
26:M:82:MET:HE3	29:A:2495:G:H4'	1.91	0.52
29:A:1428:C:N4	29:A:1570:A:OP2	2.33	0.52
29:A:1435:G:H2'	29:A:1436:G:H8	1.75	0.52
29:A:2027:G:H2'	29:A:2028:U:C6	2.44	0.52
7:J:21:THR:HG23	7:J:61:LYS:HB3	1.92	0.52
7:J:108:MET:HE1	29:A:1138:G:N3	2.25	0.52
12:R:49:ILE:HG22	12:R:54:VAL:HG23	1.92	0.52
27:H:71:LYS:HE2	27:H:108:VAL:HG11	1.92	0.52
29:A:745:G:O2'	29:A:748:G:H1'	2.09	0.52
29:A:1406:U:H2'	29:A:1407:G:C8	2.45	0.52
29:A:1965:C:H5''	29:A:1966:A:H2'	1.92	0.52
29:A:2372:U:H2'	29:A:2373:G:H8	1.73	0.52
29:A:2819:G:H2'	29:A:2821:A:N7	2.24	0.52
6:G:11:PRO:HG2	6:G:79:THR:HG21	1.91	0.51
29:A:171:U:H2'	29:A:172:A:C8	2.42	0.51
29:A:1748:C:H2'	29:A:1749:A:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:33:LEU:HD11	29:A:2286:G:C8	2.45	0.51
23:2:1:MET:N	29:A:1620:G:O4'	2.42	0.51
29:A:48:G:H22	29:A:177:G:P	2.32	0.51
29:A:2802:G:H2'	29:A:2803:G:H8	1.75	0.51
2:C:121:ALA:HB3	2:C:129:LEU:HD13	1.90	0.51
29:A:1390:U:O4	29:A:1395:A:N7	2.44	0.51
29:A:1736:U:H3'	29:A:1737:G:C8	2.46	0.51
29:A:2182:U:H2'	29:A:2183:A:H8	1.75	0.51
11:Q:49:ARG:O	11:Q:53:LYS:NZ	2.43	0.51
27:H:117:LEU:HG	27:H:120:GLY:HA2	1.92	0.51
29:A:576:U:H2'	29:A:577:G:H8	1.75	0.51
3:D:118:PHE:O	29:A:1654:A:O2'	2.26	0.51
18:X:49:ARG:NH2	29:A:1364:G:OP2	2.40	0.51
18:X:64:ASP:OD1	18:X:65:THR:N	2.43	0.51
20:Z:8:GLN:NE2	20:Z:10:ARG:O	2.37	0.51
20:Z:15:ARG:O	20:Z:20:LYS:NZ	2.43	0.51
29:A:196:A:H61	29:A:831:G:N2	2.09	0.51
29:A:1137:G:H2'	29:A:1138:G:C8	2.45	0.51
29:A:1138:G:H2'	29:A:1139:G:O4'	2.09	0.51
25:P:112:ARG:HH11	25:P:114:ASN:HD21	1.57	0.51
29:A:807:U:H2'	29:A:808:G:H8	1.75	0.51
29:A:1281:G:H2'	29:A:1282:U:H6	1.74	0.51
29:A:1417:C:H2'	29:A:1418:G:O4'	2.10	0.51
29:A:1830:C:H2'	29:A:1831:G:C8	2.45	0.51
4:E:147:LEU:HB2	4:E:183:PHE:HD1	1.74	0.51
8:L:63:LYS:HE2	29:A:2394:C:H5''	1.92	0.51
23:2:43:THR:HG23	23:2:45:SER:H	1.76	0.51
25:P:23:ASP:OD1	25:P:89:GLY:N	2.42	0.51
29:A:639:U:H2'	29:A:640:C:C6	2.46	0.51
29:A:1000:A:OP2	29:A:1154:G:N1	2.31	0.51
29:A:2008:C:H2'	29:A:2009:A:H8	1.74	0.51
29:A:2076:U:OP2	29:A:2238:G:N2	2.37	0.51
29:A:2333:A:H5'	29:A:2335:A:H1'	1.93	0.51
29:A:2781:A:H5''	29:A:2782:G:H5'	1.91	0.51
32:3:30:HIS:C	32:3:32:LEU:H	2.17	0.51
27:H:94:ILE:HG23	27:H:98:ASP:HB2	1.93	0.51
28:d:23:LYS:HA	28:d:23:LYS:HE2	1.92	0.51
29:A:5:A:H2'	29:A:6:A:C8	2.45	0.51
29:A:459:U:H2'	29:A:460:A:H8	1.76	0.51
29:A:758:C:H2'	29:A:759:G:C8	2.46	0.51
29:A:1406:U:H2'	29:A:1407:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2385:C:H2'	29:A:2386:A:C8	2.46	0.51
3:D:159:LYS:NZ	29:A:2512:C:O2'	2.33	0.51
19:Y:19:LEU:HB3	19:Y:23:ARG:NH2	2.26	0.51
29:A:2291:U:O2'	29:A:2374:C:O2	2.27	0.51
29:A:2836:U:H2'	29:A:2837:A:C8	2.46	0.51
29:A:2853:C:H2'	29:A:2854:G:C8	2.45	0.51
30:B:60:C:H2'	30:B:61:G:H8	1.75	0.51
30:B:78:A:H62	30:B:98:G:H21	1.58	0.51
2:C:257:ARG:NH1	2:C:263:ASP:OD2	2.43	0.51
9:N:44:LEU:HD22	9:N:113:ILE:HD13	1.92	0.51
29:A:910:A:H2'	29:A:911:A:C8	2.45	0.51
29:A:1589:U:H2'	29:A:1590:A:H8	1.76	0.51
29:A:2788:C:H2'	29:A:2789:C:C6	2.46	0.51
12:R:27:ILE:HG21	12:R:63:VAL:HG21	1.93	0.50
28:d:13:THR:OG1	28:d:23:LYS:NZ	2.43	0.50
29:A:758:C:H2'	29:A:759:G:H8	1.75	0.50
29:A:951:C:N4	29:A:952:G:O6	2.44	0.50
29:A:2836:U:H2'	29:A:2837:A:H8	1.77	0.50
31:9:218:ILE:HG23	31:9:220:GLY:H	1.75	0.50
4:E:21:ARG:O	4:E:114:ARG:NH1	2.39	0.50
19:Y:47:ARG:NH1	29:A:61:C:OP2	2.45	0.50
29:A:69:C:O2	29:A:73:A:O2'	2.23	0.50
29:A:414:C:H2'	29:A:415:A:C8	2.46	0.50
29:A:2065:C:H2'	29:A:2066:C:H6	1.76	0.50
29:A:2131:U:H5'	29:A:2132:U:H5''	1.91	0.50
29:A:2463:C:H2'	29:A:2464:G:H8	1.76	0.50
29:A:2514:U:H2'	29:A:2515:C:C6	2.47	0.50
5:F:97:GLU:OE2	28:d:25:ARG:NH2	2.45	0.50
6:G:94:ARG:HA	6:G:127:GLN:HE22	1.76	0.50
9:N:24:MET:HG3	9:N:44:LEU:HD12	1.93	0.50
12:R:49:ILE:O	12:R:49:ILE:HG13	2.12	0.50
12:R:97:LYS:HE2	12:R:97:LYS:HA	1.93	0.50
16:V:30:ILE:HG12	16:V:91:PHE:HB2	1.92	0.50
16:V:50:MET:HB2	16:V:53:LYS:HZ2	1.76	0.50
25:P:21:PRO:HG3	25:P:49:ILE:HD13	1.93	0.50
26:M:38:ARG:HG2	26:M:98:PRO:HD3	1.92	0.50
29:A:145:C:H2'	29:A:146:A:C8	2.46	0.50
29:A:1518:C:H2'	29:A:1519:G:H8	1.75	0.50
29:A:1798:U:O2'	29:A:1802:A:N3	2.38	0.50
29:A:2698:U:H2'	29:A:2699:C:C6	2.47	0.50
2:C:129:LEU:HD12	2:C:133:ASN:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:U:5:ARG:HG2	15:U:6:ARG:H	1.76	0.50
29:A:750:A:OP1	29:A:1615:C:N4	2.38	0.50
29:A:828:U:H4'	29:A:831:G:N1	2.26	0.50
29:A:1997:C:H2'	29:A:1998:A:H8	1.75	0.50
29:A:2460:U:H2'	29:A:2461:A:H8	1.74	0.50
19:Y:32:ALA:HB2	19:Y:37:LEU:HD13	1.93	0.50
22:1:5:ARG:NH1	22:1:23:THR:O	2.45	0.50
29:A:1432:G:H2'	29:A:1433:A:H8	1.75	0.50
29:A:2233:U:H2'	29:A:2234:G:C8	2.43	0.50
29:A:2241:A:H2'	29:A:2242:G:C8	2.47	0.50
29:A:2841:C:H2'	29:A:2842:G:H8	1.76	0.50
29:A:2848:G:H1'	29:A:2868:A:H61	1.77	0.50
3:D:114:LYS:NZ	29:A:2723:C:OP1	2.43	0.50
29:A:465:G:N2	29:A:684:G:H1'	2.27	0.50
29:A:825:A:N1	29:A:833:A:N6	2.59	0.50
29:A:911:A:H5''	29:A:912:C:H5''	1.94	0.50
29:A:1672:A:C6	29:A:2582:G:H5'	2.46	0.50
29:A:2329:U:H2'	29:A:2330:G:C8	2.45	0.50
29:A:2855:C:H2'	29:A:2856:A:C8	2.46	0.50
22:1:34:GLU:OE1	22:1:49:LYS:NZ	2.35	0.50
29:A:581:C:H2'	29:A:582:A:C8	2.46	0.50
29:A:639:U:H2'	29:A:640:C:H6	1.77	0.50
5:F:118:ALA:O	5:F:166:ARG:NH1	2.44	0.50
6:G:87:GLN:HE22	6:G:164:ALA:HA	1.76	0.50
29:A:689:A:N3	29:A:779:U:O2'	2.42	0.50
29:A:954:G:H1	29:A:963:U:H3	1.59	0.50
29:A:1042:G:H1	29:A:1113:U:H3	1.59	0.50
29:A:2505:G:N2	29:A:2576:G:N7	2.60	0.50
29:A:2594:C:H2'	29:A:2595:G:C8	2.46	0.50
2:C:106:PRO:HG2	2:C:109:LEU:HB2	1.94	0.50
3:D:149:ASN:O	3:D:152:PRO:HD2	2.12	0.50
12:R:65:ALA:HB3	12:R:95:ASP:HB2	1.94	0.50
12:R:71:LYS:HA	12:R:90:ARG:HG2	1.93	0.50
14:T:38:ALA:HB3	14:T:81:LYS:HD2	1.93	0.50
15:U:32:LYS:HB3	15:U:63:ALA:HB1	1.94	0.50
18:X:53:LYS:NZ	29:A:373:U:OP2	2.36	0.50
19:Y:6:LEU:HD23	19:Y:56:LEU:HD11	1.93	0.50
29:A:23:G:H2'	29:A:24:G:C8	2.46	0.50
29:A:881:G:H2'	29:A:882:G:H8	1.76	0.50
29:A:1026:G:H2'	29:A:1027:A:H8	1.77	0.50
29:A:1073:A:H3'	29:A:1074:G:H5''	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1710:G:H2'	29:A:1711:A:C8	2.47	0.50
29:A:2656:U:N3	29:A:2665:A:C8	2.77	0.50
16:V:45:ASP:HA	16:V:48:MET:HE2	1.94	0.49
20:Z:50:VAL:HB	20:Z:53:MET:SD	2.52	0.49
26:M:57:VAL:O	26:M:60:GLN:HG3	2.12	0.49
29:A:580:U:H2'	29:A:581:C:C6	2.47	0.49
29:A:1539:U:H2'	29:A:1540:G:C8	2.46	0.49
13:S:31:GLN:O	13:S:35:ILE:HG12	2.13	0.49
21:O:51:ARG:NH1	21:O:53:VAL:HG12	2.27	0.49
29:A:1102:C:H2'	29:A:1103:A:H8	1.77	0.49
29:A:1582:C:O2'	29:A:1585:C:N3	2.42	0.49
8:L:121:THR:HG22	8:L:141:LYS:HB3	1.94	0.49
16:V:56:PHE:CE1	16:V:61:LEU:HD11	2.48	0.49
21:O:52:LYS:HD3	21:O:55:ALA:HA	1.94	0.49
29:A:226:A:H1'	29:A:230:G:N2	2.28	0.49
29:A:308:G:N2	29:A:477:A:N7	2.59	0.49
29:A:351:C:H2'	29:A:352:A:C8	2.47	0.49
29:A:417:C:H2'	29:A:418:C:C6	2.47	0.49
29:A:2036:C:H2'	29:A:2037:A:H8	1.77	0.49
29:A:2685:G:H21	29:A:2726:A:N6	2.10	0.49
5:F:16:MET:HE3	5:F:24:VAL:HA	1.93	0.49
29:A:175:G:H2'	29:A:176:A:C8	2.47	0.49
29:A:631:A:OP2	32:3:22:LYS:NZ	2.43	0.49
29:A:1267:U:H2'	29:A:1268:A:H8	1.77	0.49
29:A:1443:U:H2'	29:A:1444:G:C8	2.46	0.49
29:A:1563:U:H2'	29:A:1564:C:C6	2.48	0.49
30:B:40:U:N3	30:B:44:G:OP2	2.44	0.49
30:B:95:U:H2'	30:B:96:G:H8	1.76	0.49
29:A:581:C:H2'	29:A:582:A:H8	1.77	0.49
29:A:767:U:H2'	29:A:768:G:H8	1.77	0.49
29:A:966:G:H4'	29:A:2271:G:H22	1.78	0.49
29:A:1748:C:H2'	29:A:1749:A:C8	2.48	0.49
2:C:151:GLY:O	2:C:155:ARG:NH1	2.32	0.49
3:D:22:ILE:HG23	3:D:190:LYS:HZ2	1.77	0.49
29:A:922:C:H2'	29:A:923:G:H8	1.76	0.49
29:A:967:U:H2'	29:A:968:C:C6	2.48	0.49
29:A:1264:A:H4'	29:A:2615:U:H5'	1.95	0.49
29:A:1378:A:O2'	29:A:1380:G:OP2	2.30	0.49
29:A:1447:C:O2'	29:A:1544:A:N3	2.42	0.49
29:A:2127:G:H2'	29:A:2128:G:C8	2.48	0.49
2:C:71:ASP:OD1	2:C:72:GLY:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:W:22:PHE:N	17:W:25:GLU:OE2	2.46	0.49
29:A:55:G:H2'	29:A:56:A:H8	1.78	0.49
29:A:230:G:H2'	29:A:231:A:H8	1.78	0.49
29:A:438:G:H2'	29:A:439:A:C8	2.48	0.49
29:A:538:A:H62	29:A:555:G:N2	2.11	0.49
29:A:1431:A:H2'	29:A:1432:G:H8	1.78	0.49
29:A:1441:G:H2'	29:A:1442:U:C6	2.48	0.49
29:A:1726:C:H2'	29:A:1727:C:C6	2.48	0.49
29:A:2109:U:N3	29:A:2110:G:O6	2.45	0.49
31:9:168:PRO:HB3	31:9:191:PHE:H	1.77	0.49
32:3:32:LEU:HD23	32:3:40:LYS:HG2	1.94	0.49
5:F:104:THR:HA	28:d:38:SER:HB3	1.95	0.49
5:F:135:ILE:HA	5:F:140:ILE:HD11	1.95	0.49
6:G:25:ILE:HG23	6:G:78:VAL:HG11	1.94	0.49
7:J:49:ASP:OD1	7:J:121:LYS:NZ	2.37	0.49
25:P:61:ARG:HE	25:P:63:ILE:HD11	1.77	0.49
29:A:953:G:O2'	29:A:2266:A:OP2	2.28	0.49
29:A:1433:A:H2'	29:A:1434:A:C8	2.47	0.49
29:A:1808:A:H3'	29:A:1809:A:C8	2.48	0.49
29:A:2441:U:OP2	29:A:2586:U:O2'	2.31	0.49
29:A:2841:C:H2'	29:A:2842:G:C8	2.48	0.49
3:D:157:LYS:HG2	29:A:2619:C:H5''	1.95	0.49
5:F:110:ILE:HG23	5:F:113:PHE:HB2	1.94	0.49
8:L:112:LEU:O	29:A:627:A:N6	2.39	0.49
29:A:1259:G:H2'	29:A:1260:A:C8	2.47	0.49
29:A:2473:U:OP1	29:A:2529:G:N2	2.45	0.49
29:A:2847:U:H2'	29:A:2848:G:O4'	2.13	0.49
8:L:132:ARG:O	8:L:135:ILE:HG22	2.13	0.49
9:N:1:MET:SD	9:N:1:MET:N	2.85	0.49
29:A:1435:G:H2'	29:A:1436:G:C8	2.47	0.49
29:A:2304:G:H22	29:A:2312:U:H3	1.60	0.49
29:A:924:G:H2'	29:A:925:A:H8	1.78	0.48
29:A:1131:G:N2	29:A:1132:U:O4	2.34	0.48
29:A:2737:G:H2'	29:A:2738:A:C8	2.48	0.48
30:B:77:U:O2	30:B:99:A:N7	2.46	0.48
2:C:107:LYS:HA	2:C:195:GLY:HA2	1.95	0.48
3:D:155:VAL:HG21	29:A:2618:G:H21	1.78	0.48
29:A:20:C:H2'	29:A:21:A:H8	1.78	0.48
29:A:249:C:O2	32:3:11:LYS:NZ	2.45	0.48
29:A:457:A:N7	29:A:472:A:N6	2.60	0.48
29:A:579:G:H2'	29:A:580:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:833:A:H2'	29:A:834:G:C8	2.48	0.48
29:A:1400:U:H2'	29:A:1401:G:H8	1.77	0.48
3:D:4:LEU:HD21	3:D:100:LEU:HD21	1.95	0.48
3:D:45:TYR:OH	29:A:2636:C:O2'	2.30	0.48
26:M:3:GLN:HG2	26:M:4:PRO:HD2	1.95	0.48
29:A:306:U:H2'	29:A:307:G:O4'	2.12	0.48
29:A:1704:C:H2'	29:A:1705:A:C8	2.48	0.48
29:A:1801:A:H5'	29:A:2203:U:H2'	1.95	0.48
29:A:2229:U:H2'	29:A:2230:G:C8	2.46	0.48
31:9:13:ALA:HB1	31:9:120:GLY:HA2	1.94	0.48
3:D:125:TRP:CD1	3:D:160:LYS:HB3	2.48	0.48
12:R:41:ILE:HB	12:R:47:VAL:HB	1.96	0.48
13:S:25:ARG:NH2	13:S:74:ILE:O	2.45	0.48
29:A:499:U:H2'	29:A:500:G:O4'	2.13	0.48
29:A:749:A:H5'	29:A:1271:G:H1'	1.93	0.48
29:A:1434:A:H2'	29:A:1435:G:H8	1.78	0.48
29:A:1918:A:O2'	29:A:1919:A:N7	2.39	0.48
29:A:2120:G:H2'	29:A:2121:G:C8	2.45	0.48
29:A:2637:U:O4	29:A:2776:A:N7	2.46	0.48
30:B:70:C:H2'	30:B:71:C:H6	1.77	0.48
3:D:151:THR:HB	3:D:152:PRO:HD3	1.96	0.48
5:F:118:ALA:HB2	5:F:177:ARG:HA	1.95	0.48
13:S:73:LYS:HB2	13:S:106:VAL:HB	1.94	0.48
29:A:864:G:O2'	29:A:914:G:O6	2.30	0.48
29:A:1038:G:H2'	29:A:1039:A:C8	2.48	0.48
29:A:1207:C:H2'	29:A:1208:C:C6	2.49	0.48
29:A:1637:A:H2'	29:A:1638:C:C6	2.48	0.48
32:3:30:HIS:O	32:3:32:LEU:N	2.45	0.48
13:S:67:ASP:OD2	13:S:68:ASP:N	2.46	0.48
14:T:22:THR:HA	14:T:25:GLU:HG2	1.95	0.48
29:A:851:C:H2'	29:A:852:U:C6	2.49	0.48
29:A:1013:C:H2'	29:A:1014:A:C8	2.49	0.48
29:A:2623:G:OP1	29:A:2826:A:O2'	2.32	0.48
30:B:29:A:H2'	30:B:30:C:C6	2.49	0.48
31:9:290:LYS:HG3	31:9:291:VAL:H	1.79	0.48
2:C:194:VAL:HG22	2:C:195:GLY:H	1.77	0.48
3:D:173:GLN:NE2	29:A:2771:C:O2'	2.42	0.48
7:J:120:ARG:NE	29:A:2780:G:OP2	2.47	0.48
29:A:87:U:H3	29:A:95:A:H61	1.60	0.48
29:A:2439:A:O2'	29:A:2600:A:OP1	2.30	0.48
2:C:74:PRO:HD2	2:C:96:LYS:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:8:LYS:NZ	3:D:195:GLY:O	2.42	0.48
6:G:175:LYS:HE2	29:A:2530:A:H5'	1.96	0.48
27:H:62:LEU:O	27:H:66:ASN:ND2	2.47	0.48
29:A:155:A:H2'	29:A:156:A:C8	2.49	0.48
29:A:946:C:H2'	29:A:947:A:C8	2.49	0.48
29:A:1495:A:H2	29:A:1578:U:H1'	1.79	0.48
29:A:1564:C:H2'	29:A:1565:C:C6	2.48	0.48
29:A:2231:U:H2'	29:A:2232:C:C6	2.49	0.48
29:A:2385:C:H2'	29:A:2386:A:H8	1.78	0.48
29:A:2824:C:H3'	29:A:2825:G:H21	1.79	0.48
6:G:37:ASN:HD22	6:G:63:GLN:CD	2.20	0.48
23:2:26:ASN:CG	29:A:682:G:H5'	2.39	0.48
29:A:877:A:O2'	29:A:900:A:N6	2.47	0.48
29:A:934:U:H2'	29:A:935:C:H6	1.79	0.48
29:A:1441:G:H2'	29:A:1442:U:H6	1.79	0.48
29:A:1444:G:H2'	29:A:1445:G:H8	1.79	0.48
29:A:1936:A:H2	29:A:1943:U:H3	1.62	0.48
29:A:2345:G:H5'	29:A:2347:C:H5'	1.96	0.48
3:D:178:VAL:HG12	3:D:179:ARG:HG3	1.95	0.48
18:X:2:ARG:NH2	29:A:1365:A:OP1	2.41	0.48
24:K:40:LYS:HD2	24:K:57:VAL:HG12	1.96	0.48
29:A:319:G:H2'	29:A:320:A:C8	2.49	0.48
29:A:539:G:H1	29:A:554:U:H3	1.61	0.48
29:A:2840:C:H2'	29:A:2841:C:H6	1.79	0.48
30:B:116:G:H2'	30:B:117:G:H8	1.79	0.48
2:C:222:THR:N	29:A:1826:G:OP1	2.47	0.47
3:D:3:GLY:HA2	3:D:101:PHE:HZ	1.79	0.47
29:A:924:G:H2'	29:A:925:A:C8	2.49	0.47
29:A:2204:G:O6	29:A:2220:U:O4	2.32	0.47
3:D:77:ARG:NH2	3:D:200:ASP:OD1	2.47	0.47
29:A:625:G:H2'	29:A:626:A:C8	2.49	0.47
29:A:1275:A:N1	29:A:1295:C:O2'	2.39	0.47
29:A:1709:U:H2'	29:A:1710:G:C8	2.49	0.47
29:A:2719:G:H4'	29:A:2846:G:H4'	1.95	0.47
14:T:8:LEU:HD11	19:Y:26:PHE:HB2	1.97	0.47
16:V:21:ARG:NH1	30:B:77:U:OP1	2.35	0.47
29:A:64:A:H2'	29:A:65:U:H6	1.79	0.47
29:A:1864:U:OP1	29:A:2410:G:O2'	2.30	0.47
29:A:2057:G:H2'	29:A:2058:A:C8	2.50	0.47
29:A:2127:G:H21	29:A:2173:A:H1'	1.79	0.47
29:A:2688:G:N1	29:A:2720:U:OP2	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2834:G:H1'	29:A:2883:A:H61	1.80	0.47
9:N:3:HIS:ND1	29:A:2820:A:H4'	2.29	0.47
14:T:61:LEU:HD11	14:T:82:LYS:HD3	1.96	0.47
24:K:80:ASP:OD2	25:P:61:ARG:NH1	2.47	0.47
29:A:155:A:H2'	29:A:156:A:H8	1.78	0.47
29:A:172:A:H2'	29:A:173:A:H8	1.79	0.47
29:A:671:C:H2'	29:A:672:C:H6	1.78	0.47
29:A:1357:C:H2'	29:A:1358:G:O4'	2.14	0.47
29:A:2470:G:H2'	29:A:2471:A:H8	1.79	0.47
30:B:6:G:H2'	30:B:7:G:C8	2.49	0.47
4:E:108:ILE:HD12	4:E:181:ILE:HD11	1.97	0.47
12:R:6:GLN:HB3	12:R:11:GLN:HG2	1.95	0.47
24:K:5:GLN:H	24:K:22:ILE:HA	1.78	0.47
25:P:55:HIS:HB3	29:A:2683:C:H5''	1.97	0.47
29:A:419:U:H2'	29:A:420:C:C6	2.48	0.47
29:A:437:U:H2'	29:A:438:G:H8	1.80	0.47
29:A:1346:G:N2	29:A:1347:A:H1'	2.29	0.47
29:A:1438:U:H2'	29:A:1439:A:C8	2.48	0.47
29:A:1520:U:H2'	29:A:1521:G:O4'	2.13	0.47
29:A:2215:C:H2'	29:A:2216:G:C8	2.49	0.47
29:A:2606:C:H2'	29:A:2607:G:H8	1.79	0.47
29:A:2818:U:H2'	29:A:2819:G:H8	1.80	0.47
13:S:3:THR:OG1	13:S:62:ASP:OD2	2.31	0.47
17:W:73:ARG:NH2	29:A:2333:A:OP2	2.47	0.47
29:A:13:A:O2'	29:A:15:G:N7	2.46	0.47
29:A:414:C:H2'	29:A:415:A:H8	1.80	0.47
29:A:589:U:H2'	29:A:590:A:H8	1.80	0.47
29:A:948:C:H2'	29:A:949:G:C8	2.49	0.47
29:A:1141:U:H4'	29:A:1142:A:O4'	2.15	0.47
29:A:1353:A:H2'	29:A:1354:A:H8	1.79	0.47
29:A:2577:A:O4'	29:A:2612:C:N4	2.48	0.47
4:E:196:VAL:HA	4:E:199:MET:HG3	1.96	0.47
15:U:38:ILE:HG21	15:U:64:ILE:HG13	1.97	0.47
27:H:47:PHE:O	27:H:51:ARG:NH1	2.48	0.47
29:A:161:A:OP2	29:A:162:U:O2'	2.28	0.47
29:A:302:C:H2'	29:A:303:G:C8	2.50	0.47
29:A:996:A:H2'	29:A:997:G:C8	2.50	0.47
29:A:1720:U:H2'	29:A:1721:G:O4'	2.14	0.47
29:A:1801:A:N6	29:A:2201:G:O2'	2.39	0.47
29:A:1930:G:N2	29:A:1969:A:O5'	2.42	0.47
29:A:2039:U:H2'	29:A:2040:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2064:C:H2'	29:A:2065:C:H6	1.80	0.47
29:A:2372:U:H2'	29:A:2373:G:C8	2.50	0.47
29:A:2636:C:H2'	29:A:2637:U:H6	1.79	0.47
32:3:32:LEU:HA	32:3:35:LYS:HE3	1.97	0.47
9:N:22:ARG:HG3	9:N:70:THR:HA	1.97	0.47
13:S:78:GLU:OE2	29:A:24:G:N2	2.47	0.47
29:A:16:C:H2'	29:A:17:G:H8	1.77	0.47
29:A:1752:C:H2'	29:A:1753:G:C8	2.50	0.47
29:A:2011:U:H2'	29:A:2012:G:O4'	2.14	0.47
29:A:2182:U:H2'	29:A:2183:A:C8	2.50	0.47
29:A:2228:G:H2'	29:A:2229:U:C6	2.50	0.47
3:D:30:GLU:OE1	3:D:33:ARG:NH2	2.47	0.47
8:L:96:LYS:HB3	8:L:103:ILE:HD13	1.96	0.47
10:O:25:ARG:NH1	30:B:8:C:O3'	2.48	0.47
11:Q:54:ARG:HD3	29:A:1155:A:H5''	1.96	0.47
13:S:77:ASP:HB3	29:A:24:G:H1'	1.95	0.47
24:K:18:ARG:NH2	24:K:45:GLU:HG2	2.30	0.47
29:A:987:C:H2'	29:A:988:A:O4'	2.15	0.47
29:A:1733:G:H2'	29:A:1734:G:C8	2.50	0.47
29:A:2066:C:H2'	29:A:2067:G:C8	2.49	0.47
29:A:2707:U:H2'	29:A:2708:G:C8	2.49	0.47
30:B:51:G:O6	30:B:52:A:N6	2.47	0.47
30:B:83:G:O6	30:B:94:A:N6	2.47	0.47
5:F:98:PHE:HA	5:F:101:ARG:HG2	1.96	0.47
6:G:2:ARG:NH1	29:A:2751:G:OP2	2.46	0.47
29:A:307:G:N2	29:A:309:A:H3'	2.30	0.47
29:A:505:A:O2'	29:A:509:C:O2'	2.26	0.47
29:A:582:A:H2'	29:A:583:G:H8	1.78	0.47
29:A:996:A:H2'	29:A:997:G:H8	1.79	0.47
29:A:1431:A:H2'	29:A:1432:G:C8	2.49	0.47
29:A:2425:A:H4'	29:A:2426:A:O5'	2.14	0.47
31:9:24:ARG:HB2	31:9:35:ASP:HB2	1.97	0.47
2:C:38:LYS:NZ	2:C:55:GLY:O	2.42	0.46
4:E:52:VAL:HB	4:E:74:LYS:HD2	1.96	0.46
29:A:630:G:N2	29:A:633:A:OP2	2.32	0.46
29:A:1079:C:H2'	29:A:1080:A:O4'	2.15	0.46
29:A:1821:A:H2'	29:A:1822:C:C6	2.50	0.46
29:A:2329:U:H2'	29:A:2330:G:H8	1.80	0.46
5:F:121:PHE:HE2	5:F:166:ARG:HH12	1.63	0.46
6:G:84:LYS:HB3	6:G:132:LEU:HB2	1.98	0.46
16:V:50:MET:O	16:V:53:LYS:NZ	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Y:26:PHE:O	19:Y:30:MET:HG2	2.15	0.46
29:A:491:G:H3'	29:A:492:A:H8	1.79	0.46
29:A:777:G:H2'	29:A:778:G:H8	1.79	0.46
29:A:1355:G:H2'	29:A:1356:G:H8	1.80	0.46
29:A:1715:G:O2'	29:A:1743:G:O6	2.29	0.46
29:A:2036:C:H2'	29:A:2037:A:C8	2.50	0.46
1:g:24:ARG:NH2	29:A:2742:G:OP1	2.33	0.46
11:Q:67:ALA:HA	11:Q:70:GLN:OE1	2.15	0.46
13:S:24:ILE:HD13	13:S:36:LEU:HD11	1.96	0.46
14:T:1:MET:C	14:T:3:ARG:HB2	2.41	0.46
16:V:9:ARG:HE	16:V:27:PRO:HB3	1.80	0.46
17:W:66:GLU:OE1	17:W:68:LYS:HG2	2.15	0.46
27:H:97:ARG:NH2	29:A:2220:U:O3'	2.49	0.46
29:A:282:A:H2'	29:A:283:G:C8	2.51	0.46
29:A:979:A:H2'	29:A:982:C:H42	1.80	0.46
29:A:1394:U:H4'	29:A:1603:A:H4'	1.97	0.46
29:A:1697:G:OP2	29:A:1698:A:O2'	2.28	0.46
29:A:1809:A:H2'	29:A:1810:A:C8	2.50	0.46
29:A:1847:A:O2'	29:A:1848:A:H8	1.99	0.46
31:9:263:ILE:HG22	31:9:267:GLU:HG3	1.98	0.46
2:C:224:MET:HE1	29:A:782:A:C4	2.50	0.46
9:N:5:LYS:NZ	29:A:2000:C:OP1	2.47	0.46
10:O:29:HIS:HB3	10:O:36:TYR:HB2	1.96	0.46
29:A:577:G:H2'	29:A:578:G:C8	2.50	0.46
29:A:1114:C:N4	29:A:1115:G:O6	2.48	0.46
29:A:2266:A:H4'	29:A:2267:A:N3	2.30	0.46
29:A:2328:A:H2'	29:A:2329:U:H6	1.80	0.46
29:A:2626:C:H2'	29:A:2627:G:C8	2.50	0.46
30:B:116:G:H2'	30:B:117:G:C8	2.50	0.46
4:E:141:MET:HG2	4:E:143:LEU:HG	1.97	0.46
25:P:5:LYS:HA	25:P:8:GLU:HB2	1.98	0.46
29:A:566:U:H2'	29:A:567:U:C6	2.50	0.46
29:A:903:C:H2'	29:A:904:G:C8	2.50	0.46
29:A:1098:A:H3'	29:A:1099:G:H8	1.81	0.46
29:A:1550:C:H2'	29:A:1551:A:H8	1.81	0.46
29:A:2446:G:N2	29:A:2449:U:O2	2.44	0.46
29:A:2845:U:H2'	29:A:2846:G:C8	2.49	0.46
6:G:59:ASP:OD1	6:G:60:GLY:N	2.40	0.46
19:Y:9:LYS:HD3	19:Y:10:SER:N	2.31	0.46
30:B:9:G:H1	30:B:111:U:H3	1.62	0.46
31:9:289:ASP:OD1	31:9:289:ASP:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:209:ALA:HA	2:C:212:TRP:CZ2	2.51	0.46
2:C:219:VAL:HG21	29:A:782:A:C8	2.50	0.46
14:T:10:VAL:HG21	14:T:42:GLU:HB3	1.97	0.46
16:V:61:LEU:N	16:V:72:VAL:O	2.46	0.46
27:H:9:VAL:HG22	27:H:10:ALA:H	1.81	0.46
29:A:67:U:C2	29:A:68:G:C8	3.03	0.46
29:A:582:A:H2'	29:A:583:G:C8	2.51	0.46
29:A:970:U:H2'	29:A:971:G:C8	2.51	0.46
29:A:1164:C:H2'	29:A:1165:A:C8	2.50	0.46
29:A:1571:A:H2'	29:A:1572:A:H8	1.81	0.46
29:A:1638:C:O2	29:A:2698:U:O2'	2.34	0.46
31:9:177:ARG:NH2	31:9:184:PRO:HD2	2.30	0.46
18:X:16:ASN:HB2	18:X:24:THR:HB	1.96	0.46
21:0:30:ASP:HB3	21:0:34:GLY:H	1.81	0.46
27:H:4:ILE:HG21	27:H:51:ARG:HH22	1.80	0.46
29:A:732:C:H2'	29:A:733:G:O4'	2.16	0.46
29:A:793:A:OP2	29:A:2071:A:O2'	2.34	0.46
29:A:1665:A:H2'	29:A:1666:G:H8	1.80	0.46
29:A:1826:G:H2'	29:A:1827:U:C6	2.51	0.46
29:A:2030:A:H4'	29:A:2031:A:H8	1.80	0.46
29:A:2047:C:O2'	29:A:2823:A:N1	2.42	0.46
29:A:2241:A:H2'	29:A:2242:G:H8	1.80	0.46
29:A:2414:G:C2	29:A:2415:G:C8	3.04	0.46
29:A:2642:G:H2'	29:A:2643:G:H8	1.81	0.46
2:C:240:GLY:O	29:A:2596:U:O2'	2.34	0.46
4:E:43:THR:HB	29:A:38:A:N3	2.31	0.46
9:N:34:ILE:HD12	29:A:1278:C:H4'	1.97	0.46
10:O:117:PHE:O	29:A:2377:A:O2'	2.34	0.46
11:Q:106:THR:O	11:Q:110:GLU:OE1	2.34	0.46
29:A:1084:A:N3	29:A:1105:U:O2'	2.48	0.46
29:A:1751:U:H2'	29:A:1752:C:C6	2.50	0.46
29:A:1862:G:H1	29:A:1880:U:H3	1.64	0.46
29:A:2364:C:H2'	29:A:2365:G:O4'	2.16	0.46
29:A:2416:C:C2	29:A:2417:C:C5	3.03	0.46
29:A:2625:G:H2'	29:A:2626:C:C6	2.51	0.46
31:9:177:ARG:NH1	31:9:182:ALA:H	2.14	0.46
31:9:306:TRP:CE3	31:9:308:ASP:HB2	2.51	0.46
29:A:24:G:H2'	29:A:25:U:C6	2.50	0.46
29:A:355:U:H2'	29:A:356:G:C8	2.51	0.46
29:A:680:C:H2'	29:A:681:G:C8	2.50	0.46
29:A:926:G:H2'	29:A:927:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2391:G:O2'	29:A:2424:C:N4	2.42	0.46
29:A:2457:U:H2'	29:A:2458:G:C8	2.50	0.46
31:9:222:ALA:HB1	31:9:268:LYS:HD2	1.98	0.46
9:N:39:PRO:HG2	29:A:1651:G:H5'	1.98	0.45
19:Y:48:ARG:NH1	29:A:76:C:OP1	2.49	0.45
24:K:7:MET:HE2	24:K:18:ARG:HB3	1.98	0.45
29:A:419:U:H2'	29:A:420:C:H6	1.82	0.45
29:A:551:G:H2'	29:A:552:U:C6	2.51	0.45
29:A:599:A:H2'	29:A:600:G:C8	2.51	0.45
29:A:695:G:H1	29:A:767:U:H3	1.62	0.45
29:A:832:U:H2'	29:A:833:A:C8	2.48	0.45
29:A:934:U:H2'	29:A:935:C:C6	2.51	0.45
30:B:6:G:H2'	30:B:7:G:H8	1.80	0.45
30:B:70:C:H2'	30:B:71:C:C6	2.51	0.45
4:E:192:ALA:HA	4:E:195:GLN:HE21	1.81	0.45
6:G:157:LYS:HE3	6:G:157:LYS:HB3	1.72	0.45
11:Q:56:PHE:HZ	29:A:536:G:H4'	1.80	0.45
19:Y:49:ASP:HA	19:Y:52:ARG:HG2	1.98	0.45
29:A:106:C:H2'	29:A:107:G:H8	1.81	0.45
29:A:301:G:O2'	29:A:302:C:O5'	2.32	0.45
29:A:523:C:H5''	29:A:540:C:O2'	2.16	0.45
29:A:558:U:H2'	29:A:559:G:H8	1.81	0.45
29:A:589:U:H2'	29:A:590:A:C8	2.51	0.45
29:A:638:G:H2'	29:A:639:U:H6	1.82	0.45
29:A:1298:C:H2'	29:A:1299:G:O4'	2.16	0.45
29:A:1496:A:H2'	29:A:1498:C:C5	2.51	0.45
29:A:1696:G:N2	29:A:1977:A:HO2'	2.12	0.45
29:A:2031:A:N3	29:A:2455:G:O2'	2.43	0.45
29:A:2460:U:O2	29:A:2493:U:N3	2.50	0.45
29:A:2731:G:H2'	29:A:2732:G:C8	2.51	0.45
7:J:95:ARG:HG2	7:J:96:ARG:HD3	1.98	0.45
12:R:27:ILE:HG23	12:R:31:GLU:OE2	2.16	0.45
29:A:2254:C:C2	29:A:2255:G:C8	3.05	0.45
29:A:2784:U:H2'	29:A:2785:C:H6	1.81	0.45
30:B:20:G:H2'	30:B:21:G:H8	1.82	0.45
3:D:194:PRO:HB3	29:A:2679:A:H4'	1.97	0.45
29:A:69:C:H2'	29:A:70:G:C8	2.50	0.45
29:A:411:G:OP2	29:A:2406:A:O2'	2.30	0.45
29:A:558:U:H2'	29:A:559:G:C8	2.52	0.45
29:A:1326:U:N3	29:A:1648:U:O2'	2.45	0.45
29:A:2357:G:N2	29:A:2360:G:OP2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2370:G:H2'	29:A:2371:G:C8	2.51	0.45
29:A:2584:U:H2'	29:A:2585:U:O4'	2.16	0.45
29:A:2623:G:H2'	29:A:2624:G:C8	2.51	0.45
32:3:15:LYS:HD2	32:3:19:GLY:HA2	1.99	0.45
5:F:16:MET:HE1	5:F:21:TYR:HB2	1.97	0.45
24:K:66:LYS:HZ3	24:K:80:ASP:HA	1.80	0.45
26:M:112:LEU:O	26:M:115:GLU:HG3	2.17	0.45
29:A:341:C:H2'	29:A:342:A:C8	2.52	0.45
29:A:364:C:H2'	29:A:365:U:C6	2.51	0.45
29:A:541:A:H2'	29:A:542:C:C6	2.51	0.45
29:A:946:C:H2'	29:A:947:A:H8	1.82	0.45
29:A:1019:U:OP1	29:A:1035:U:O2'	2.26	0.45
29:A:1841:U:H2'	29:A:1842:G:H8	1.81	0.45
29:A:2023:C:H2'	29:A:2024:G:H8	1.80	0.45
29:A:2315:G:H2'	29:A:2316:G:H8	1.81	0.45
30:B:9:G:C2	30:B:10:G:C8	3.04	0.45
27:H:1:MET:SD	27:H:3:VAL:N	2.89	0.45
29:A:55:G:H2'	29:A:56:A:C8	2.52	0.45
29:A:599:A:H2'	29:A:600:G:H8	1.82	0.45
29:A:807:U:H2'	29:A:808:G:C8	2.51	0.45
29:A:1442:U:H2'	29:A:1443:U:C6	2.52	0.45
29:A:1825:U:H2'	29:A:1826:G:C8	2.50	0.45
29:A:2028:U:O4	29:A:2033:A:N7	2.49	0.45
8:L:23:ILE:HG12	12:R:82:HIS:NE2	2.32	0.45
29:A:247:G:O2'	29:A:386:G:N1	2.48	0.45
29:A:2065:C:H2'	29:A:2066:C:C6	2.51	0.45
29:A:2340:A:H2'	29:A:2341:G:H8	1.81	0.45
32:3:27:ASN:O	32:3:32:LEU:HD21	2.17	0.45
2:C:256:THR:OG1	29:A:1797:G:O2'	2.34	0.45
9:N:106:ASP:OD1	29:A:1649:G:O2'	2.27	0.45
11:Q:20:ALA:HB2	11:Q:38:VAL:HG23	1.99	0.45
27:H:30:LEU:HB3	27:H:36:ALA:HB3	1.99	0.45
28:d:36:VAL:HG11	28:d:41:HIS:CD2	2.51	0.45
29:A:451:U:O2	29:A:453:A:N6	2.50	0.45
29:A:1231:U:H2'	29:A:1232:G:H8	1.81	0.45
29:A:1389:G:H2'	29:A:1390:U:C6	2.52	0.45
29:A:1464:G:H2'	29:A:1465:G:C8	2.52	0.45
29:A:2081:U:H2'	29:A:2082:A:C8	2.49	0.45
6:G:54:ARG:HH11	6:G:57:TYR:HE2	1.65	0.45
25:P:26:GLU:HB2	25:P:86:LYS:NZ	2.32	0.45
29:A:191:A:O2'	29:A:678:C:O2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:243:U:OP2	32:3:7:ARG:NH1	2.50	0.45
29:A:1005:C:H2'	29:A:1006:C:C6	2.52	0.45
29:A:1222:U:H2'	29:A:1223:G:C8	2.52	0.45
29:A:1361:G:H2'	29:A:1362:C:H6	1.81	0.45
29:A:1409:U:H2'	29:A:1410:G:H8	1.82	0.45
29:A:2339:C:H2'	29:A:2340:A:H8	1.82	0.45
7:J:80:HIS:ND1	7:J:81:ILE:HG22	2.32	0.45
7:J:101:ILE:HD13	7:J:124:VAL:HG21	1.99	0.45
29:A:639:U:C2	29:A:640:C:C5	3.05	0.45
29:A:727:A:H2'	29:A:728:G:C8	2.52	0.45
29:A:1028:A:OP2	29:A:1126:A:N6	2.50	0.45
29:A:1744:A:H3'	29:A:1745:A:H8	1.82	0.45
29:A:2291:U:H2'	29:A:2292:U:C6	2.52	0.45
29:A:2487:G:H2'	29:A:2488:G:C8	2.52	0.45
29:A:2602:A:H8	31:9:33:GLY:HA2	1.81	0.45
29:A:2804:U:H2'	29:A:2805:C:H6	1.82	0.45
30:B:22:U:H3	30:B:61:G:H1	1.63	0.45
30:B:32:U:H2'	30:B:33:G:C8	2.52	0.45
5:F:14:LYS:O	5:F:17:THR:N	2.49	0.44
27:H:112:LYS:HZ3	29:A:2220:U:H5'	1.82	0.44
29:A:1131:G:O2'	29:A:2025:C:O2'	2.35	0.44
29:A:1434:A:H2'	29:A:1435:G:C8	2.52	0.44
29:A:1436:G:O2'	29:A:1515:A:N1	2.44	0.44
29:A:1874:C:H2'	29:A:1875:G:O4'	2.17	0.44
2:C:204:LEU:HB3	2:C:209:ALA:HB3	1.99	0.44
7:J:102:GLU:HA	7:J:105:VAL:HB	1.98	0.44
9:N:28:LEU:HD22	9:N:44:LEU:HD21	1.99	0.44
18:X:54:GLY:O	18:X:58:ILE:HG23	2.17	0.44
29:A:63:A:H2'	29:A:64:A:H8	1.82	0.44
29:A:296:U:H2'	29:A:297:G:C8	2.53	0.44
29:A:743:A:H2'	29:A:744:U:C6	2.51	0.44
29:A:1404:C:H2'	29:A:1405:U:H6	1.83	0.44
29:A:1630:A:N1	29:A:1637:A:N6	2.66	0.44
29:A:2636:C:H2'	29:A:2637:U:C6	2.52	0.44
30:B:30:C:H2'	30:B:31:C:O4'	2.18	0.44
3:D:184:ARG:HB3	3:D:186:LEU:HD13	1.99	0.44
18:X:4:CYS:SG	18:X:7:THR:OG1	2.70	0.44
21:O:14:MET:HE3	29:A:2045:C:H4'	2.00	0.44
24:K:25:LEU:HD22	29:A:2562:U:H4'	1.99	0.44
27:H:26:ALA:O	27:H:30:LEU:HB2	2.17	0.44
28:d:11:GLU:OE1	28:d:25:ARG:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:404:A:H4'	29:A:405:U:O5'	2.16	0.44
29:A:724:U:H2'	29:A:725:G:O4'	2.18	0.44
29:A:796:C:H2'	29:A:797:G:H8	1.80	0.44
29:A:940:G:H2'	29:A:941:A:O4'	2.16	0.44
29:A:1219:U:H2'	29:A:1220:G:C8	2.53	0.44
29:A:1850:G:H2'	29:A:1851:U:C6	2.52	0.44
29:A:2087:G:H2'	29:A:2088:A:H8	1.83	0.44
13:S:92:ARG:O	29:A:1614:A:N6	2.46	0.44
24:K:2:ILE:HD12	24:K:8:LEU:HD21	2.00	0.44
29:A:526:A:O2'	29:A:2043:C:O2	2.32	0.44
29:A:595:C:H2'	29:A:596:U:C6	2.53	0.44
29:A:819:A:N6	29:A:1189:A:H1'	2.33	0.44
29:A:2710:C:H2'	29:A:2711:A:C8	2.53	0.44
29:A:2774:C:H2'	29:A:2775:G:O4'	2.17	0.44
29:A:2888:C:H2'	29:A:2889:C:C6	2.53	0.44
31:9:173:SER:N	35:9:402:GNP:O2B	2.39	0.44
31:9:192:THR:N	35:9:402:GNP:O3G	2.39	0.44
10:O:99:TYR:O	10:O:103:VAL:HB	2.18	0.44
14:T:6:ARG:NH2	14:T:37:ASP:OD2	2.51	0.44
29:A:500:G:N1	29:A:503:A:OP2	2.39	0.44
29:A:513:A:H4'	29:A:1217:U:H5'	1.99	0.44
29:A:579:G:H2'	29:A:580:U:H6	1.83	0.44
29:A:967:U:H2'	29:A:968:C:H6	1.81	0.44
29:A:1352:U:H1'	29:A:1570:A:H2	1.82	0.44
29:A:1558:C:H4'	29:A:1559:U:H3'	1.99	0.44
29:A:1749:A:H2'	29:A:1750:G:H8	1.82	0.44
29:A:2582:G:C2	29:A:2583:G:C8	3.05	0.44
5:F:32:LYS:HD3	5:F:91:ARG:HH22	1.82	0.44
5:F:150:GLY:HA3	29:A:2305:U:N3	2.33	0.44
8:L:111:ILE:HG21	29:A:636:G:C6	2.53	0.44
10:O:45:SER:OG	30:B:9:G:O2'	2.28	0.44
13:S:58:ALA:O	13:S:62:ASP:HB2	2.18	0.44
27:H:5:LEU:HD22	27:H:13:GLY:HA3	1.98	0.44
29:A:201:C:H2'	29:A:202:U:C6	2.53	0.44
29:A:594:U:H2'	29:A:595:C:C6	2.53	0.44
29:A:596:U:H2'	29:A:597:G:C8	2.52	0.44
29:A:680:C:H2'	29:A:681:G:H8	1.83	0.44
3:D:48:ILE:HG21	3:D:90:PHE:HB2	1.99	0.44
3:D:149:ASN:HB3	29:A:2572:A:OP2	2.18	0.44
13:S:46:LEU:O	13:S:50:VAL:HG23	2.17	0.44
24:K:7:MET:HE3	24:K:8:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:M:42:THR:HG22	26:M:93:VAL:HG12	2.00	0.44
29:A:16:C:H2'	29:A:17:G:C8	2.52	0.44
29:A:25:U:H2'	29:A:26:G:O4'	2.18	0.44
29:A:686:U:H2'	29:A:788:A:N1	2.33	0.44
29:A:781:A:H5''	29:A:782:A:N7	2.32	0.44
29:A:1066:U:N3	29:A:1069:A:OP2	2.51	0.44
29:A:2130:U:O2'	29:A:2134:A:O4'	2.34	0.44
29:A:2368:C:H2'	29:A:2369:A:H8	1.83	0.44
29:A:2639:A:H2'	29:A:2640:G:O4'	2.18	0.44
29:A:2705:A:O2'	29:A:2852:G:OP1	2.28	0.44
3:D:170:VAL:HG11	29:A:2679:A:H5'	2.00	0.44
8:L:56:PRO:HG2	8:L:59:ARG:HD3	2.00	0.44
12:R:5:PHE:HA	12:R:39:LEU:HD23	2.00	0.44
29:A:1047:G:N2	29:A:1110:G:O2'	2.47	0.44
29:A:1136:G:H2'	29:A:1137:G:C8	2.52	0.44
29:A:1954:G:O2'	29:A:1956:U:O4	2.28	0.44
16:V:20:LEU:HD11	16:V:41:GLU:CD	2.43	0.44
29:A:438:G:H2'	29:A:439:A:H8	1.83	0.44
29:A:475:C:H4'	29:A:510:C:H5'	1.99	0.44
29:A:1987:A:H2'	29:A:1988:G:H8	1.82	0.44
29:A:2099:U:H2'	29:A:2100:G:H8	1.83	0.44
29:A:2554:U:H2'	29:A:2555:U:C6	2.53	0.44
29:A:2798:U:O2	29:A:2799:A:N6	2.51	0.44
29:A:2808:G:O2'	29:A:2890:G:O6	2.29	0.44
30:B:74:U:H2'	30:B:75:G:O4'	2.18	0.44
3:D:7:LYS:NZ	3:D:198:GLY:O	2.46	0.43
16:V:21:ARG:HA	16:V:25:LYS:O	2.18	0.43
24:K:31:ARG:NH2	29:A:2676:C:OP1	2.48	0.43
26:M:53:MET:HE3	26:M:120:ALA:HB2	2.00	0.43
29:A:78:U:O4	29:A:108:G:O6	2.35	0.43
29:A:287:G:H1	29:A:353:C:H42	1.66	0.43
29:A:1026:G:H2'	29:A:1027:A:C8	2.52	0.43
29:A:1654:A:H2'	29:A:1655:A:H8	1.84	0.43
29:A:2018:G:H2'	29:A:2019:A:H8	1.83	0.43
29:A:2412:A:H2'	29:A:2413:G:O4'	2.18	0.43
29:A:2470:G:H2'	29:A:2471:A:C8	2.53	0.43
30:B:20:G:H2'	30:B:21:G:C8	2.53	0.43
30:B:40:U:H3'	30:B:41:G:H4'	1.99	0.43
30:B:60:C:H2'	30:B:61:G:C8	2.52	0.43
12:R:36:ALA:HA	12:R:58:VAL:HG23	2.00	0.43
29:A:172:A:H2'	29:A:173:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:285:G:N2	29:A:355:U:O2	2.39	0.43
29:A:289:G:H2'	29:A:290:U:C6	2.53	0.43
29:A:693:A:O2'	29:A:1353:A:N3	2.52	0.43
29:A:1407:G:H2'	29:A:1408:G:H8	1.82	0.43
29:A:1722:A:N6	29:A:1738:G:H1'	2.33	0.43
29:A:2647:U:H2'	29:A:2648:G:H8	1.83	0.43
31:9:249:PRO:HG2	31:9:253:THR:H	1.82	0.43
5:F:33:ILE:HD12	5:F:155:ILE:HD12	2.00	0.43
6:G:83:THR:HG22	6:G:133:LYS:HE3	2.00	0.43
7:J:37:ARG:NH2	29:A:1007:C:H5''	2.33	0.43
7:J:95:ARG:NH2	29:A:2768:U:O2'	2.51	0.43
9:N:29:VAL:HG13	9:N:75:ILE:HD12	1.98	0.43
29:A:800:A:O4'	29:A:802:A:H5'	2.19	0.43
29:A:813:U:H2'	29:A:814:C:H6	1.83	0.43
29:A:1040:A:N1	29:A:1115:G:N2	2.66	0.43
29:A:1107:G:H2'	29:A:1108:U:C6	2.54	0.43
29:A:1229:C:H2'	29:A:1230:A:C8	2.53	0.43
29:A:1234:U:H2'	29:A:1235:G:O4'	2.18	0.43
29:A:1550:C:H2'	29:A:1551:A:C8	2.53	0.43
29:A:1833:C:O2'	29:A:1969:A:N1	2.47	0.43
29:A:1967:C:H2'	29:A:1968:G:O4'	2.18	0.43
29:A:1987:A:H2'	29:A:1988:G:C8	2.53	0.43
29:A:2315:G:H2'	29:A:2316:G:C8	2.53	0.43
29:A:2785:C:H2'	29:A:2786:U:H6	1.84	0.43
29:A:2848:G:H1'	29:A:2868:A:N6	2.32	0.43
29:A:2875:C:H2'	29:A:2876:G:C8	2.53	0.43
2:C:151:GLY:O	2:C:155:ARG:HD2	2.18	0.43
17:W:73:ARG:HH22	29:A:2333:A:P	2.40	0.43
19:Y:18:LEU:CD2	19:Y:23:ARG:HH12	2.32	0.43
23:2:3:ARG:HD3	23:2:3:ARG:HA	1.87	0.43
26:M:66:ARG:NH2	29:A:906:U:O2'	2.52	0.43
28:d:17:SER:OG	28:d:35:ASP:O	2.30	0.43
29:A:311:A:N6	29:A:329:G:OP1	2.51	0.43
29:A:1112:G:H2'	29:A:1113:U:C6	2.54	0.43
29:A:1258:U:H2'	29:A:1259:G:C8	2.54	0.43
29:A:1779:U:H5''	29:A:1780:A:H5''	2.00	0.43
29:A:1880:U:H2'	29:A:1881:C:C6	2.53	0.43
29:A:2027:G:H2'	29:A:2028:U:H6	1.81	0.43
29:A:2087:G:H2'	29:A:2088:A:C8	2.54	0.43
29:A:2589:A:H2'	29:A:2590:A:H8	1.83	0.43
29:A:2804:U:H2'	29:A:2805:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:49:LEU:HD13	6:G:71:LEU:HD23	2.01	0.43
8:L:78:ARG:HH11	29:A:627:A:H5''	1.83	0.43
9:N:4:ARG:NH2	29:A:2875:C:OP1	2.51	0.43
28:d:36:VAL:HG11	28:d:41:HIS:HD2	1.84	0.43
29:A:106:C:H2'	29:A:107:G:C8	2.53	0.43
29:A:128:C:H2'	29:A:129:C:H6	1.82	0.43
29:A:253:C:H2'	29:A:254:G:O4'	2.18	0.43
29:A:923:G:H2'	29:A:924:G:H8	1.83	0.43
29:A:1219:U:H2'	29:A:1220:G:H8	1.84	0.43
29:A:1544:A:H2'	29:A:1545:A:C8	2.54	0.43
29:A:2139:U:H2'	29:A:2140:G:H8	1.82	0.43
2:C:224:MET:HE1	29:A:782:A:N3	2.34	0.43
29:A:1444:G:H2'	29:A:1445:G:C8	2.54	0.43
2:C:131:MET:HA	2:C:134:ILE:HD12	2.00	0.43
9:N:71:ARG:HA	9:N:71:ARG:HD2	1.77	0.43
14:T:59:ASN:HB2	14:T:84:TYR:HB2	2.01	0.43
16:V:50:MET:HB2	16:V:53:LYS:NZ	2.33	0.43
27:H:97:ARG:HH21	27:H:112:LYS:NZ	2.17	0.43
29:A:634:C:H2'	29:A:635:C:H6	1.83	0.43
29:A:753:A:H2'	29:A:754:U:C6	2.54	0.43
29:A:817:C:H2'	29:A:818:G:O4'	2.19	0.43
29:A:1168:G:H2'	29:A:1169:A:C8	2.53	0.43
29:A:1412:U:H2'	29:A:1413:A:C8	2.53	0.43
29:A:1721:G:N1	29:A:1738:G:N7	2.67	0.43
29:A:1827:U:H2'	29:A:1828:G:O4'	2.19	0.43
29:A:2289:G:H2'	29:A:2290:G:H8	1.84	0.43
29:A:2505:G:H1'	29:A:2506:U:OP2	2.18	0.43
30:B:115:A:H2'	30:B:116:G:H8	1.82	0.43
31:9:74:ALA:HB3	31:9:78:CYS:HB2	2.00	0.43
4:E:192:ALA:HA	4:E:195:GLN:HG2	2.01	0.43
24:K:42:THR:HG22	24:K:57:VAL:HG22	2.01	0.43
24:K:97:THR:O	24:K:98:ARG:NE	2.49	0.43
29:A:196:A:N6	29:A:831:G:H21	2.17	0.43
29:A:324:A:N6	29:A:339:U:O4'	2.51	0.43
29:A:596:U:H2'	29:A:597:G:H8	1.84	0.43
29:A:629:G:H5''	29:A:650:C:O2'	2.18	0.43
29:A:1395:A:O2'	29:A:1396:U:H3'	2.19	0.43
29:A:1562:U:H2'	29:A:1563:U:C6	2.53	0.43
29:A:1562:U:H2'	29:A:1563:U:H6	1.84	0.43
29:A:1869:G:N2	29:A:1871:A:O2'	2.52	0.43
29:A:2064:C:H2'	29:A:2065:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2794:C:H2'	29:A:2795:C:C6	2.54	0.43
2:C:207:ALA:HB2	29:A:1790:C:O2'	2.19	0.43
8:L:47:ARG:HH22	8:L:58:TYR:HH	1.67	0.43
10:O:31:THR:HG21	30:B:28:C:H5''	2.00	0.43
11:Q:32:ARG:O	29:A:1252:G:N2	2.52	0.43
29:A:181:A:H1'	29:A:435:C:H5'	1.99	0.43
29:A:183:C:H1'	29:A:432:A:C2	2.54	0.43
29:A:475:C:N3	29:A:479:A:N7	2.67	0.43
29:A:675:A:N3	29:A:2443:C:O2'	2.49	0.43
29:A:685:A:O2'	29:A:773:U:O4	2.30	0.43
29:A:976:G:H2'	29:A:977:G:H8	1.84	0.43
29:A:1139:G:H2'	29:A:1140:C:C6	2.54	0.43
29:A:2515:C:H2'	29:A:2516:A:C8	2.48	0.43
3:D:164:GLN:O	3:D:165:MET:HE2	2.19	0.43
5:F:13:LYS:O	5:F:17:THR:HG23	2.18	0.43
13:S:23:LEU:HD22	21:O:23:ALA:HB2	2.01	0.43
13:S:96:ILE:HD11	29:A:2012:G:H4'	2.01	0.43
27:H:54:LEU:O	27:H:57:LYS:HG3	2.19	0.43
29:A:78:U:H2'	29:A:79:C:C6	2.54	0.43
29:A:1207:C:H2'	29:A:1208:C:H6	1.83	0.43
29:A:1291:C:H2'	29:A:1292:G:C8	2.53	0.43
29:A:1424:G:H2'	29:A:1425:G:C8	2.54	0.43
29:A:1440:U:H2'	29:A:1441:G:C8	2.53	0.43
29:A:1476:U:H2'	29:A:1477:A:H8	1.84	0.43
29:A:1796:U:H2'	29:A:1797:G:C8	2.53	0.43
29:A:1858:A:H2'	29:A:1859:U:O4'	2.19	0.43
31:9:17:GLY:N	31:9:40:GLY:O	2.49	0.43
31:9:189:TYR:CE2	31:9:192:THR:HA	2.54	0.43
3:D:68:PHE:HB3	3:D:73:VAL:O	2.19	0.42
3:D:155:VAL:O	29:A:2618:G:O2'	2.34	0.42
5:F:4:HIS:HD1	5:F:96:TRP:CD1	2.36	0.42
5:F:60:SER:HA	5:F:98:PHE:CZ	2.54	0.42
6:G:174:LYS:O	6:G:174:LYS:HD2	2.19	0.42
9:N:35:LYS:HD3	9:N:112:TYR:CZ	2.54	0.42
14:T:50:LEU:HD23	19:Y:26:PHE:CZ	2.54	0.42
26:M:55:ARG:HA	26:M:59:ARG:NH1	2.34	0.42
29:A:76:C:H2'	29:A:77:G:H8	1.84	0.42
29:A:244:A:H2'	29:A:245:G:O4'	2.19	0.42
29:A:1169:A:H2'	29:A:1170:C:C6	2.54	0.42
29:A:1429:G:H2'	29:A:1430:G:C8	2.53	0.42
29:A:1738:G:O2'	29:A:1739:A:H8	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2220:U:H2'	29:A:2221:G:H8	1.83	0.42
29:A:2547:A:OP2	29:A:2566:A:O2'	2.29	0.42
29:A:2783:U:H2'	29:A:2784:U:H6	1.84	0.42
29:A:2840:C:H2'	29:A:2841:C:C6	2.53	0.42
30:B:63:C:H2'	30:B:64:G:C8	2.54	0.42
2:C:136:VAL:HG13	2:C:163:ILE:HG22	2.01	0.42
29:A:528:A:H2'	29:A:529:A:H5''	2.00	0.42
29:A:797:G:H2'	29:A:798:G:C8	2.54	0.42
29:A:1276:A:N6	29:A:1645:G:O6	2.52	0.42
29:A:1299:G:O6	29:A:1639:C:H5''	2.19	0.42
29:A:1733:G:H2'	29:A:1734:G:H8	1.83	0.42
29:A:1965:C:OP1	29:A:1966:A:O2'	2.34	0.42
29:A:2047:C:H2'	29:A:2048:G:C8	2.53	0.42
29:A:2411:A:H2'	29:A:2412:A:H8	1.84	0.42
2:C:79:ARG:NH2	2:C:81:GLU:OE2	2.52	0.42
2:C:181:ARG:HG3	2:C:266:ILE:HG12	2.01	0.42
5:F:146:ASP:OD1	5:F:146:ASP:N	2.51	0.42
16:V:21:ARG:HE	16:V:87:GLN:HA	1.84	0.42
19:Y:37:LEU:HD23	19:Y:37:LEU:O	2.19	0.42
29:A:134:G:H2'	29:A:135:U:C6	2.55	0.42
29:A:239:C:N3	29:A:259:G:N1	2.67	0.42
29:A:1106:G:H2'	29:A:1107:G:H8	1.84	0.42
29:A:1336:A:H2'	29:A:1337:G:C8	2.54	0.42
29:A:1941:C:H1'	31:9:131:LYS:O	2.19	0.42
29:A:2018:G:H2'	29:A:2019:A:C8	2.55	0.42
29:A:2316:G:H2'	29:A:2317:A:C8	2.54	0.42
29:A:2888:C:H2'	29:A:2889:C:H6	1.84	0.42
30:B:72:G:N2	30:B:104:A:H62	2.15	0.42
3:D:11:MET:HB2	3:D:25:THR:HA	2.00	0.42
8:L:78:ARG:HG2	8:L:113:ALA:HB3	2.01	0.42
10:O:87:ILE:O	10:O:87:ILE:HG22	2.19	0.42
11:Q:52:ARG:NH2	29:A:994:C:OP1	2.52	0.42
29:A:48:G:N2	29:A:177:G:OP2	2.52	0.42
29:A:136:G:H2'	29:A:137:U:C6	2.54	0.42
29:A:173:A:H2'	29:A:174:U:C6	2.55	0.42
29:A:1198:U:H2'	29:A:1199:U:C6	2.54	0.42
29:A:1361:G:H2'	29:A:1362:C:C6	2.54	0.42
7:J:30:THR:HG21	29:A:1012:U:O4	2.20	0.42
16:V:43:ASP:OD2	16:V:46:LYS:NZ	2.40	0.42
26:M:44:ARG:HA	26:M:47:GLU:OE2	2.20	0.42
27:H:97:ARG:HH22	29:A:2221:G:P	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:634:C:H2'	29:A:635:C:C6	2.54	0.42
29:A:641:U:O4	29:A:647:G:O6	2.37	0.42
29:A:2700:A:H2'	29:A:2701:U:C6	2.54	0.42
29:A:2815:C:H2'	29:A:2816:G:C8	2.54	0.42
29:A:2881:U:H2'	29:A:2882:A:C8	2.54	0.42
30:B:115:A:H2'	30:B:116:G:C8	2.53	0.42
12:R:80:ARG:NH1	29:A:572:A:OP2	2.53	0.42
29:A:12:U:O2	29:A:2626:C:H4'	2.20	0.42
29:A:128:C:H2'	29:A:129:C:C6	2.53	0.42
29:A:593:U:H2'	29:A:594:U:H6	1.83	0.42
29:A:600:G:H2'	29:A:601:C:H6	1.84	0.42
29:A:903:C:H2'	29:A:904:G:H8	1.83	0.42
29:A:1022:G:N7	29:A:1140:C:N4	2.68	0.42
29:A:1346:G:N1	29:A:1601:G:C6	2.87	0.42
29:A:2086:U:H2'	29:A:2087:G:C8	2.54	0.42
2:C:77:VAL:HG22	2:C:113:ASP:H	1.84	0.42
2:C:169:ALA:HA	27:H:123:ARG:HH22	1.84	0.42
5:F:64:PRO:HA	5:F:88:VAL:HG22	2.02	0.42
7:J:15:TRP:CE2	7:J:135:GLN:HG2	2.54	0.42
8:L:132:ARG:HG3	8:L:142:ILE:HG13	2.02	0.42
18:X:41:SER:OG	18:X:42:GLU:OE1	2.26	0.42
18:X:60:LYS:HE2	29:A:372:G:C8	2.54	0.42
20:Z:46:MET:O	20:Z:50:VAL:HG22	2.19	0.42
29:A:1:G:H2'	29:A:2:G:H8	1.84	0.42
29:A:18:U:H2'	29:A:19:A:C8	2.54	0.42
29:A:65:U:H2'	29:A:66:C:H6	1.85	0.42
29:A:202:U:H2'	29:A:203:A:O4'	2.19	0.42
29:A:395:U:O2'	29:A:396:G:N7	2.39	0.42
29:A:543:G:C2	29:A:551:G:C2	3.08	0.42
29:A:769:U:H2'	29:A:770:G:C8	2.55	0.42
29:A:812:C:H5''	29:A:1250:G:O2'	2.20	0.42
29:A:947:A:H2'	29:A:948:C:C6	2.54	0.42
29:A:1319:C:H2'	29:A:1320:C:C6	2.54	0.42
29:A:1464:G:H2'	29:A:1465:G:H8	1.85	0.42
29:A:1630:A:H2'	29:A:1631:G:O4'	2.19	0.42
29:A:1675:C:H2'	29:A:1676:A:O4'	2.19	0.42
29:A:1727:C:H2'	29:A:1728:C:O4'	2.20	0.42
29:A:1771:C:H2'	29:A:1772:A:C8	2.54	0.42
29:A:2691:C:H2'	29:A:2692:G:C8	2.54	0.42
29:A:2788:C:H2'	29:A:2789:C:H6	1.84	0.42
5:F:62:GLN:HG3	5:F:94:ARG:NH2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:140:ILE:HG13	6:G:141:GLY:N	2.35	0.42
10:O:30:ARG:HA	10:O:35:ILE:HG22	2.01	0.42
14:T:61:LEU:HB3	29:A:1341:G:H5'	2.02	0.42
16:V:78:GLN:OE1	30:B:76:G:O2'	2.31	0.42
21:O:16:ARG:NE	29:A:1266:G:OP2	2.48	0.42
29:A:481:G:N1	29:A:507:A:H1'	2.35	0.42
29:A:1267:U:H2'	29:A:1268:A:C8	2.54	0.42
29:A:1409:U:H2'	29:A:1410:G:C8	2.55	0.42
29:A:2391:G:C6	29:A:2427:C:H1'	2.55	0.42
29:A:2464:G:H2'	29:A:2465:C:C6	2.55	0.42
29:A:2644:G:N2	29:A:2733:A:OP2	2.52	0.42
29:A:131:A:H2'	29:A:132:G:C8	2.54	0.42
29:A:282:A:N6	29:A:359:G:O6	2.52	0.42
29:A:492:A:H2'	29:A:493:G:O4'	2.20	0.42
29:A:565:C:H2'	29:A:566:U:C6	2.55	0.42
29:A:1007:C:OP2	29:A:1008:A:O2'	2.27	0.42
29:A:1153:C:H2'	29:A:1154:G:O4'	2.19	0.42
29:A:1300:G:H4'	29:A:1301:A:H5''	2.01	0.42
29:A:1308:A:H2'	29:A:1309:G:O4'	2.20	0.42
29:A:1475:G:H1'	29:A:1476:U:H5	1.85	0.42
29:A:2216:G:H2'	29:A:2217:G:H8	1.85	0.42
29:A:2773:C:H2'	29:A:2774:C:H6	1.84	0.42
2:C:227:VAL:HG11	29:A:784:G:C4	2.55	0.42
4:E:48:THR:O	4:E:52:VAL:HG23	2.20	0.42
8:L:93:ASN:C	8:L:95:LEU:H	2.28	0.42
11:Q:10:ARG:NH2	29:A:28:A:N3	2.68	0.42
18:X:38:TRP:CG	27:H:32:PRO:HA	2.55	0.42
19:Y:1:MET:O	19:Y:4:LYS:NZ	2.51	0.42
21:O:42:ILE:HD12	21:O:46:GLY:HA2	2.02	0.42
22:1:22:THR:HG21	29:A:2286:G:H1	1.85	0.42
29:A:538:A:H62	29:A:555:G:H21	1.67	0.42
29:A:1106:G:H2'	29:A:1107:G:C8	2.55	0.42
29:A:1268:A:H1'	29:A:2013:A:H61	1.84	0.42
29:A:1790:C:H2'	29:A:1791:A:C5	2.55	0.42
29:A:1947:C:H2'	29:A:1948:G:H8	1.84	0.42
29:A:2616:C:H2'	29:A:2617:U:C6	2.54	0.42
31:9:132:SER:OG	31:9:133:SER:N	2.53	0.42
2:C:13:ARG:NH2	29:A:1693:U:O2'	2.52	0.41
6:G:25:ILE:HG13	6:G:78:VAL:HG21	2.01	0.41
6:G:34:ARG:HD2	6:G:74:MET:HE1	2.02	0.41
8:L:32:GLY:HA2	29:A:1190:G:H5''	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:69:ARG:C	9:N:71:ARG:H	2.28	0.41
24:K:99:ILE:HG13	24:K:115:ILE:HG23	2.02	0.41
28:d:31:ASP:OD1	28:d:31:ASP:N	2.52	0.41
29:A:146:A:H2'	29:A:147:C:C6	2.54	0.41
29:A:299:A:H2'	29:A:300:A:C4	2.55	0.41
29:A:611:C:H2'	29:A:612:G:O4'	2.20	0.41
29:A:678:C:H2'	29:A:679:C:C6	2.55	0.41
29:A:1398:C:H2'	29:A:1399:C:H6	1.85	0.41
29:A:1442:U:H2'	29:A:1443:U:H6	1.85	0.41
29:A:1749:A:H2'	29:A:1750:G:C8	2.55	0.41
29:A:2314:A:H2'	29:A:2315:G:H8	1.85	0.41
29:A:2362:C:OP1	32:3:39:ARG:HD2	2.20	0.41
7:J:15:TRP:HE3	7:J:55:ILE:HD11	1.86	0.41
9:N:2:ARG:HH22	29:A:2819:G:P	2.43	0.41
14:T:11:LEU:HD11	14:T:32:LEU:HD13	2.02	0.41
20:Z:26:LEU:HD23	20:Z:26:LEU:HA	1.91	0.41
24:K:12:ASP:N	24:K:12:ASP:OD1	2.53	0.41
28:d:16:CYS:HA	28:d:34:LEU:HB2	2.02	0.41
29:A:603:A:N6	29:A:655:A:O4'	2.53	0.41
29:A:640:C:H2'	29:A:641:U:C6	2.55	0.41
29:A:1440:U:H2'	29:A:1441:G:H8	1.86	0.41
29:A:2766:A:N3	29:A:2766:A:H2'	2.35	0.41
30:B:113:C:H2'	30:B:114:C:C6	2.55	0.41
8:L:128:THR:HG23	8:L:131:ALA:H	1.85	0.41
10:O:84:GLU:HG2	10:O:85:LYS:HD3	2.02	0.41
13:S:51:LEU:O	13:S:55:ILE:HG12	2.20	0.41
15:U:88:ASP:O	15:U:90:LYS:N	2.54	0.41
24:K:24:VAL:HG13	24:K:39:ILE:HG22	2.01	0.41
26:M:66:ARG:NH1	26:M:104:GLU:OE2	2.53	0.41
29:A:569:U:H2'	29:A:570:G:O4'	2.20	0.41
29:A:600:G:H2'	29:A:601:C:C6	2.55	0.41
29:A:1067:A:H2'	29:A:1067:A:N3	2.34	0.41
29:A:1130:U:N3	29:A:2025:C:OP1	2.50	0.41
29:A:1259:G:H2'	29:A:1260:A:H8	1.85	0.41
29:A:1380:G:H2'	29:A:1381:G:H8	1.84	0.41
29:A:1398:C:H2'	29:A:1399:C:C6	2.55	0.41
29:A:2037:A:H2'	29:A:2038:G:C8	2.55	0.41
29:A:2062:A:H2'	29:A:2063:C:C6	2.55	0.41
29:A:2193:G:H2'	29:A:2194:U:C6	2.55	0.41
29:A:2193:G:H2'	29:A:2194:U:H6	1.85	0.41
29:A:2290:G:H2'	29:A:2291:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:259:ALA:HB1	31:9:304:LEU:HD21	2.02	0.41
31:9:290:LYS:HA	31:9:290:LYS:HD3	1.81	0.41
2:C:200:MET:N	2:C:200:MET:SD	2.93	0.41
14:T:6:ARG:O	14:T:10:VAL:HG23	2.20	0.41
24:K:92:GLU:O	24:K:93:GLN:NE2	2.54	0.41
29:A:32:C:H2'	29:A:33:C:C6	2.55	0.41
29:A:922:C:H2'	29:A:923:G:C8	2.55	0.41
29:A:1652:A:H2'	29:A:1653:G:O4'	2.21	0.41
29:A:1665:A:H2'	29:A:1666:G:C8	2.54	0.41
29:A:1680:U:H2'	29:A:1681:G:O4'	2.21	0.41
29:A:1909:C:H2'	29:A:1910:G:C8	2.55	0.41
29:A:2645:G:H3'	29:A:2646:C:H5'	2.02	0.41
1:g:13:ASN:HD22	1:g:29:ALA:HB2	1.86	0.41
4:E:148:ILE:HB	4:E:169:VAL:HG22	2.01	0.41
8:L:91:ASP:N	8:L:91:ASP:OD1	2.52	0.41
13:S:28:LYS:H	13:S:31:GLN:HE21	1.69	0.41
16:V:72:VAL:HB	16:V:91:PHE:HB3	2.02	0.41
29:A:151:C:H2'	29:A:152:A:H8	1.85	0.41
29:A:418:C:H2'	29:A:419:U:C6	2.56	0.41
29:A:487:C:H2'	29:A:488:G:O4'	2.19	0.41
29:A:679:C:H2'	29:A:680:C:C6	2.55	0.41
29:A:2292:U:H2'	29:A:2293:G:C8	2.55	0.41
29:A:2533:U:H2'	29:A:2534:A:O4'	2.20	0.41
29:A:2543:G:H2'	29:A:2544:G:C8	2.55	0.41
29:A:2889:C:H2'	29:A:2890:G:O4'	2.21	0.41
2:C:12:ARG:HA	2:C:15:VAL:HG23	2.02	0.41
3:D:59:ARG:HG3	29:A:2830:C:OP1	2.21	0.41
5:F:65:LEU:HD11	30:B:41:G:C8	2.55	0.41
5:F:169:LEU:HB3	5:F:174:PHE:HB3	2.02	0.41
11:Q:90:ASP:OD1	11:Q:90:ASP:N	2.51	0.41
24:K:10:VAL:HG21	24:K:16:ALA:O	2.20	0.41
29:A:242:G:N2	29:A:255:A:OP2	2.36	0.41
29:A:393:C:C2	29:A:394:C:C5	3.09	0.41
29:A:540:C:N4	29:A:541:A:H62	2.18	0.41
29:A:598:U:H2'	29:A:599:A:H8	1.84	0.41
29:A:809:G:H2'	29:A:810:U:C6	2.55	0.41
29:A:858:G:H3'	29:A:859:G:C8	2.55	0.41
29:A:1387:A:H5'	29:A:1469:A:H1'	2.03	0.41
29:A:1667:G:O2'	29:A:1991:U:O4	2.38	0.41
29:A:1966:A:N3	29:A:2592:G:O2'	2.51	0.41
29:A:2247:A:H2'	29:A:2248:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2368:C:H2'	29:A:2369:A:C8	2.56	0.41
29:A:2462:C:H2'	29:A:2463:C:C6	2.56	0.41
29:A:2508:G:H5'	31:9:76:ARG:HH22	1.86	0.41
29:A:2560:A:H2'	29:A:2561:U:C6	2.55	0.41
29:A:2816:G:H2'	29:A:2817:U:H6	1.84	0.41
1:g:36:ARG:HG2	1:g:37:GLN:H	1.85	0.41
2:C:176:ARG:HA	2:C:176:ARG:HD2	1.87	0.41
6:G:100:ASN:O	6:G:100:ASN:OD1	2.39	0.41
19:Y:21:LEU:O	19:Y:25:GLN:HB3	2.21	0.41
29:A:671:C:H2'	29:A:672:C:C6	2.55	0.41
29:A:1264:A:O5'	29:A:1265:A:H2'	2.20	0.41
29:A:2128:G:H2'	29:A:2129:C:C6	2.55	0.41
29:A:2413:G:C4	29:A:2414:G:C8	3.09	0.41
29:A:2425:A:H5''	29:A:2427:C:O4'	2.21	0.41
29:A:2549:G:H2'	29:A:2550:G:C8	2.53	0.41
4:E:105:LEU:HD23	4:E:200:LEU:HD13	2.02	0.41
5:F:63:LYS:H	28:d:6:HIS:CE1	2.39	0.41
27:H:10:ALA:O	27:H:12:LEU:HD23	2.21	0.41
29:A:19:A:H2'	29:A:20:C:C6	2.56	0.41
29:A:413:C:H2'	29:A:414:C:C6	2.55	0.41
29:A:592:A:H2'	29:A:593:U:C6	2.56	0.41
29:A:593:U:H2'	29:A:594:U:C6	2.56	0.41
29:A:638:G:H2'	29:A:639:U:C6	2.56	0.41
29:A:1437:C:O2'	29:A:1516:G:O2'	2.27	0.41
29:A:1841:U:C2	29:A:1842:G:C8	3.08	0.41
29:A:2191:A:H2'	29:A:2192:U:H6	1.84	0.41
29:A:2283:C:OP2	29:A:2389:G:O2'	2.37	0.41
29:A:2644:G:O6	29:A:2771:C:N4	2.54	0.41
31:9:157:MET:HE1	31:9:234:HIS:HA	2.03	0.41
2:C:55:GLY:H	29:A:692:C:P	2.44	0.41
2:C:56:GLY:HA2	2:C:212:TRP:HA	2.02	0.41
2:C:218:THR:O	29:A:1789:A:H5''	2.21	0.41
3:D:124:ARG:NE	3:D:165:MET:HE3	2.35	0.41
5:F:127:TYR:CE1	5:F:169:LEU:HD21	2.56	0.41
7:J:57:LEU:HD21	7:J:130:HIS:HB3	2.03	0.41
8:L:29:LYS:HB2	12:R:82:HIS:CD2	2.56	0.41
8:L:57:LEU:HD13	8:L:60:ARG:HH11	1.86	0.41
14:T:2:ILE:HG12	14:T:49:LYS:HE3	2.03	0.41
14:T:38:ALA:HB1	14:T:43:ILE:HD11	2.03	0.41
21:0:30:ASP:HB3	21:0:34:GLY:N	2.35	0.41
29:A:7:G:H2'	29:A:8:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:243:U:H2'	29:A:244:A:C8	2.55	0.41
29:A:367:G:C6	29:A:368:A:C6	3.09	0.41
29:A:963:U:H2'	29:A:964:C:C6	2.56	0.41
29:A:1592:C:H2'	29:A:1593:A:C8	2.56	0.41
29:A:1826:G:H2'	29:A:1827:U:H6	1.86	0.41
29:A:2017:U:O2'	29:A:2019:A:OP2	2.35	0.41
29:A:2166:U:O4	29:A:2170:A:N6	2.46	0.41
29:A:2411:A:H2'	29:A:2412:A:C8	2.56	0.41
31:9:306:TRP:CD1	31:9:306:TRP:H	2.39	0.41
4:E:146:VAL:HG21	4:E:187:VAL:HG23	2.03	0.41
5:F:118:ALA:HB1	5:F:166:ARG:CZ	2.50	0.41
9:N:37:THR:HA	9:N:109:PRO:O	2.21	0.41
15:U:24:VAL:HA	15:U:35:VAL:HG22	2.02	0.41
17:W:37:ARG:HH12	29:A:2262:U:H5''	1.86	0.41
18:X:14:GLY:HA3	18:X:28:PHE:HE2	1.86	0.41
19:Y:9:LYS:NZ	19:Y:11:VAL:HG23	2.36	0.41
29:A:64:A:H2'	29:A:65:U:C6	2.55	0.41
29:A:116:C:H2'	29:A:117:G:O4'	2.21	0.41
29:A:592:A:HO2'	32:3:63:TYR:HH	1.66	0.41
29:A:640:C:C2	29:A:641:U:C5	3.08	0.41
29:A:1880:U:H2'	29:A:1881:C:H6	1.85	0.41
29:A:2615:U:H2'	29:A:2616:C:C6	2.56	0.41
30:B:33:G:H2'	30:B:34:A:C8	2.56	0.41
5:F:26:GLN:HG3	30:B:57:A:O2'	2.20	0.40
15:U:81:ARG:HH11	29:A:300:A:P	2.44	0.40
25:P:51:ASN:O	29:A:2845:U:H5''	2.21	0.40
26:M:29:GLY:HA2	26:M:106:ASP:OD2	2.20	0.40
29:A:29:U:H2'	29:A:30:G:H8	1.85	0.40
29:A:116:C:H1'	29:A:127:A:N3	2.36	0.40
29:A:175:G:H2'	29:A:176:A:H8	1.84	0.40
29:A:518:G:H2'	29:A:519:U:C6	2.57	0.40
29:A:594:U:H2'	29:A:595:C:H6	1.86	0.40
29:A:660:C:H2'	29:A:661:A:H8	1.87	0.40
29:A:910:A:H1'	29:A:2264:C:O2'	2.21	0.40
29:A:1213:A:H4'	29:A:1238:G:H21	1.85	0.40
29:A:2292:U:H2'	29:A:2293:G:H8	1.86	0.40
29:A:2514:U:H2'	29:A:2515:C:H6	1.86	0.40
32:3:25:HIS:HD1	32:3:43:LEU:HD23	1.85	0.40
5:F:137:PHE:HE2	5:F:151:LEU:HD22	1.86	0.40
7:J:81:ILE:HD11	29:A:2514:U:H4'	2.03	0.40
10:O:43:ASN:OD1	10:O:44:GLY:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:S:109:ASP:OD2	13:S:109:ASP:N	2.53	0.40
14:T:8:LEU:HD21	19:Y:21:LEU:O	2.21	0.40
15:U:14:THR:OG1	29:A:310:A:OP1	2.37	0.40
29:A:225:C:H2'	29:A:226:A:O4'	2.22	0.40
29:A:554:U:H2'	29:A:555:G:O4'	2.20	0.40
29:A:1233:C:H2'	29:A:1234:U:H6	1.86	0.40
29:A:1837:C:O2'	29:A:1927:A:N3	2.41	0.40
29:A:2255:G:C6	29:A:2256:G:C5	3.09	0.40
29:A:2464:G:H2'	29:A:2465:C:H6	1.86	0.40
29:A:2567:G:H2'	29:A:2568:U:C6	2.57	0.40
29:A:2895:G:H2'	29:A:2896:C:C6	2.55	0.40
31:9:256:VAL:HA	31:9:300:ILE:HD11	2.03	0.40
2:C:77:VAL:HG11	2:C:109:LEU:HD21	2.02	0.40
2:C:229:HIS:CD2	2:C:246:PRO:HB3	2.56	0.40
6:G:72:ASN:C	6:G:72:ASN:HD22	2.29	0.40
8:L:21:ARG:HD3	8:L:21:ARG:HA	1.91	0.40
9:N:38:LEU:HD23	9:N:109:PRO:HB2	2.03	0.40
11:Q:58:GLN:HA	11:Q:61:ILE:HG22	2.03	0.40
16:V:10:LYS:HD2	16:V:11:GLU:HB2	2.04	0.40
17:W:52:ASP:OD1	17:W:54:THR:OG1	2.37	0.40
19:Y:22:LEU:HD23	19:Y:23:ARG:HD3	2.03	0.40
29:A:63:A:H2'	29:A:64:A:C8	2.55	0.40
29:A:170:U:H2'	29:A:171:U:C6	2.56	0.40
29:A:197:A:H62	29:A:2430:A:H2'	1.86	0.40
29:A:1257:C:H2'	29:A:1258:U:C6	2.57	0.40
29:A:1649:G:H2'	29:A:1650:A:H8	1.87	0.40
29:A:2191:A:H2'	29:A:2192:U:C6	2.56	0.40
29:A:2313:C:H2'	29:A:2314:A:C8	2.54	0.40
2:C:211:ARG:NH2	29:A:764:A:N3	2.69	0.40
3:D:4:LEU:HD23	3:D:101:PHE:CZ	2.56	0.40
5:F:59:ILE:HD13	5:F:139:GLU:HB2	2.03	0.40
10:O:81:ARG:HA	10:O:84:GLU:CD	2.47	0.40
11:Q:54:ARG:HH11	29:A:1155:A:H5''	1.87	0.40
23:2:21:ARG:O	23:2:27:GLY:HA3	2.22	0.40
26:M:11:LYS:HZ2	26:M:86:LYS:HB3	1.87	0.40
29:A:206:U:C2	29:A:207:A:C8	3.09	0.40
29:A:1282:U:H2'	29:A:1283:G:O4'	2.22	0.40
29:A:1387:A:H2'	29:A:1388:G:C8	2.57	0.40
29:A:2243:U:H2'	29:A:2244:U:C6	2.55	0.40
29:A:2543:G:H2'	29:A:2544:G:H8	1.87	0.40
29:A:2881:U:H2'	29:A:2882:A:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:B:95:U:H2'	30:B:96:G:C8	2.55	0.40
30:B:106:G:H2'	30:B:107:G:O4'	2.20	0.40
31:9:217:LEU:HD11	31:9:265:GLU:OE2	2.21	0.40
2:C:155:ARG:HB2	29:A:1818:U:H2'	2.03	0.40
2:C:211:ARG:HD2	2:C:211:ARG:HA	1.89	0.40
14:T:58:VAL:HG22	14:T:85:VAL:HG22	2.03	0.40
15:U:73:ASN:HD21	15:U:98:ASN:ND2	2.20	0.40
18:X:11:PRO:HB2	18:X:27:ARG:HH21	1.85	0.40
29:A:169:G:H2'	29:A:170:U:C6	2.56	0.40
29:A:287:G:O6	29:A:354:A:N6	2.55	0.40
29:A:359:G:H2'	29:A:360:U:C6	2.56	0.40
29:A:521:U:H2'	29:A:522:A:H8	1.87	0.40
29:A:549:G:H5''	29:A:550:C:C6	2.57	0.40
29:A:971:G:H2'	29:A:972:A:O4'	2.22	0.40
29:A:1254:A:H5''	29:A:1255:U:H5''	2.04	0.40
29:A:1380:G:H2'	29:A:1381:G:C8	2.56	0.40
29:A:1462:C:C2	29:A:1463:C:C5	3.09	0.40
29:A:1742:U:H2'	29:A:1743:G:O4'	2.21	0.40
29:A:2240:U:H2'	29:A:2241:A:H8	1.87	0.40
29:A:2437:G:H2'	29:A:2438:U:C6	2.56	0.40
29:A:2845:U:H2'	29:A:2846:G:H8	1.86	0.40
30:B:19:C:H2'	30:B:20:G:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	g	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
2	C	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
3	D	207/209 (99%)	195 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	E	189/201 (94%)	180 (95%)	9 (5%)	0	100	100
5	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
6	G	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
7	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
8	L	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
9	N	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
10	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
11	Q	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
12	R	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
13	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
14	T	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
15	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
16	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
17	W	74/85 (87%)	71 (96%)	3 (4%)	0	100	100
18	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
19	Y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
20	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
21	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
22	1	48/55 (87%)	48 (100%)	0	0	100	100
23	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
24	K	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
25	P	111/115 (96%)	108 (97%)	3 (3%)	0	100	100
26	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
27	H	147/149 (99%)	131 (89%)	16 (11%)	0	100	100
28	d	45/70 (64%)	44 (98%)	1 (2%)	0	100	100
31	9	336/390 (86%)	321 (96%)	15 (4%)	0	100	100
32	3	62/65 (95%)	59 (95%)	1 (2%)	2 (3%)	3	25
All	All	3538/3720 (95%)	3370 (95%)	166 (5%)	2 (0%)	49	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	3	31	ILE

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Mol	Chain	Res	Type
32	3	32	LEU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	g	34/34 (100%)	34 (100%)	0	100	100
2	C	216/218 (99%)	216 (100%)	0	100	100
3	D	164/164 (100%)	164 (100%)	0	100	100
4	E	159/165 (96%)	159 (100%)	0	100	100
5	F	148/150 (99%)	148 (100%)	0	100	100
6	G	137/138 (99%)	137 (100%)	0	100	100
7	J	116/116 (100%)	115 (99%)	1 (1%)	70	76
8	L	103/103 (100%)	103 (100%)	0	100	100
9	N	100/100 (100%)	100 (100%)	0	100	100
10	O	86/87 (99%)	86 (100%)	0	100	100
11	Q	89/90 (99%)	89 (100%)	0	100	100
12	R	84/84 (100%)	84 (100%)	0	100	100
13	S	93/93 (100%)	93 (100%)	0	100	100
14	T	80/84 (95%)	80 (100%)	0	100	100
15	U	83/85 (98%)	83 (100%)	0	100	100
16	V	78/78 (100%)	78 (100%)	0	100	100
17	W	57/63 (90%)	57 (100%)	0	100	100
18	X	67/68 (98%)	67 (100%)	0	100	100
19	Y	55/55 (100%)	55 (100%)	0	100	100
20	Z	48/49 (98%)	48 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	45 (100%)	0	100	100
23	2	38/38 (100%)	38 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	K	103/104 (99%)	103 (100%)	0	100	100
25	P	98/100 (98%)	98 (100%)	0	100	100
26	M	109/109 (100%)	108 (99%)	1 (1%)	70	76
27	H	114/114 (100%)	114 (100%)	0	100	100
28	d	43/62 (69%)	43 (100%)	0	100	100
31	9	273/321 (85%)	273 (100%)	0	100	100
32	3	51/52 (98%)	51 (100%)	0	100	100
All	All	2918/3021 (97%)	2916 (100%)	2 (0%)	87	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	J	128	ASN
26	M	60	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	g	37	GLN
2	C	142	ASN
2	C	152	GLN
3	D	36	GLN
3	D	134	HIS
4	E	195	GLN
5	F	126	ASN
6	G	21	GLN
6	G	47	ASN
7	J	136	GLN
11	Q	36	GLN
13	S	31	GLN
15	U	73	ASN
21	0	3	GLN
24	K	5	GLN
25	P	14	GLN
27	H	73	ASN
28	d	41	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A	2895/2904 (99%)	390 (13%)	9 (0%)
30	B	118/119 (99%)	9 (7%)	0
All	All	3013/3023 (99%)	399 (13%)	9 (0%)

All (399) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A	10	A
29	A	12	U
29	A	14	A
29	A	27	G
29	A	46	G
29	A	51	G
29	A	63	A
29	A	71	A
29	A	74	A
29	A	75	G
29	A	84	A
29	A	102	U
29	A	103	A
29	A	118	A
29	A	120	U
29	A	125	A
29	A	138	U
29	A	139	U
29	A	140	C
29	A	142	A
29	A	160	A
29	A	163	C
29	A	181	A
29	A	196	A
29	A	199	A
29	A	215	G
29	A	216	A
29	A	221	A
29	A	222	A
29	A	230	G
29	A	233	A
29	A	248	G
29	A	255	A
29	A	265	A

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Mol	Chain	Res	Type
29	A	266	G
29	A	267	C
29	A	271	G
29	A	272	A
29	A	278	A
29	A	302	C
29	A	311	A
29	A	329	G
29	A	330	A
29	A	331	C
29	A	352	A
29	A	353	C
29	A	371	A
29	A	372	G
29	A	386	G
29	A	396	G
29	A	401	A
29	A	404	A
29	A	405	U
29	A	411	G
29	A	424	G
29	A	430	A
29	A	451	U
29	A	480	A
29	A	481	G
29	A	491	G
29	A	504	A
29	A	505	A
29	A	510	C
29	A	532	A
29	A	543	G
29	A	544	C
29	A	546	U
29	A	547	A
29	A	548	G
29	A	550	C
29	A	563	A
29	A	573	U
29	A	575	A
29	A	586	A
29	A	603	A
29	A	613	A

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Mol	Chain	Res	Type
29	A	615	U
29	A	621	A
29	A	627	A
29	A	637	A
29	A	646	U
29	A	647	G
29	A	654	A
29	A	655	A
29	A	686	U
29	A	726	G
29	A	729	G
29	A	730	A
29	A	747	U
29	A	752	A
29	A	764	A
29	A	775	G
29	A	776	G
29	A	782	A
29	A	784	G
29	A	785	G
29	A	789	A
29	A	792	A
29	A	805	G
29	A	812	C
29	A	819	A
29	A	827	U
29	A	828	U
29	A	830	G
29	A	845	A
29	A	846	U
29	A	847	U
29	A	857	G
29	A	860	U
29	A	878	A
29	A	884	U
29	A	885	C
29	A	896	A
29	A	907	G
29	A	910	A
29	A	915	C
29	A	931	U
29	A	941	A

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Mol	Chain	Res	Type
29	A	946	C
29	A	953	G
29	A	961	C
29	A	973	A
29	A	974	G
29	A	983	A
29	A	995	C
29	A	996	A
29	A	1009	A
29	A	1012	U
29	A	1013	C
29	A	1022	G
29	A	1026	G
29	A	1027	A
29	A	1033	U
29	A	1044	C
29	A	1046	A
29	A	1047	G
29	A	1058	U
29	A	1061	U
29	A	1066	U
29	A	1068	G
29	A	1069	A
29	A	1070	A
29	A	1071	G
29	A	1074	G
29	A	1081	U
29	A	1087	G
29	A	1089	A
29	A	1098	A
29	A	1101	U
29	A	1110	G
29	A	1112	G
29	A	1116	G
29	A	1132	U
29	A	1133	A
29	A	1135	C
29	A	1136	G
29	A	1141	U
29	A	1142	A
29	A	1157	G
29	A	1171	G

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Mol	Chain	Res	Type
29	A	1172	C
29	A	1173	U
29	A	1175	A
29	A	1176	U
29	A	1180	U
29	A	1212	G
29	A	1225	G
29	A	1236	G
29	A	1238	G
29	A	1250	G
29	A	1253	A
29	A	1256	G
29	A	1266	G
29	A	1272	A
29	A	1294	U
29	A	1300	G
29	A	1301	A
29	A	1302	A
29	A	1314	C
29	A	1321	A
29	A	1325	U
29	A	1329	U
29	A	1345	C
29	A	1365	A
29	A	1368	G
29	A	1378	A
29	A	1379	U
29	A	1383	A
29	A	1416	G
29	A	1419	A
29	A	1420	A
29	A	1428	C
29	A	1452	G
29	A	1453	A
29	A	1458	U
29	A	1461	C
29	A	1467	U
29	A	1482	G
29	A	1490	A
29	A	1493	C
29	A	1504	A
29	A	1515	A

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Mol	Chain	Res	Type
29	A	1523	U
29	A	1524	G
29	A	1533	C
29	A	1535	A
29	A	1548	A
29	A	1555	G
29	A	1556	C
29	A	1566	A
29	A	1569	A
29	A	1583	A
29	A	1585	C
29	A	1603	A
29	A	1607	C
29	A	1608	A
29	A	1634	A
29	A	1646	C
29	A	1647	U
29	A	1648	U
29	A	1654	A
29	A	1667	G
29	A	1674	G
29	A	1715	G
29	A	1729	U
29	A	1730	C
29	A	1732	C
29	A	1736	U
29	A	1737	G
29	A	1738	G
29	A	1764	C
29	A	1773	A
29	A	1791	A
29	A	1800	C
29	A	1801	A
29	A	1808	A
29	A	1816	C
29	A	1829	A
29	A	1870	C
29	A	1914	C
29	A	1926	U
29	A	1927	A
29	A	1930	G
29	A	1931	U

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Mol	Chain	Res	Type
29	A	1937	A
29	A	1944	U
29	A	1955	U
29	A	1967	C
29	A	1970	A
29	A	1971	U
29	A	1972	G
29	A	1991	U
29	A	1992	G
29	A	1993	U
29	A	1997	C
29	A	2013	A
29	A	2021	C
29	A	2022	U
29	A	2023	C
29	A	2025	C
29	A	2030	A
29	A	2031	A
29	A	2043	C
29	A	2055	C
29	A	2056	G
29	A	2060	A
29	A	2061	G
29	A	2062	A
29	A	2069	G
29	A	2072	C
29	A	2093	G
29	A	2096	C
29	A	2102	G
29	A	2110	G
29	A	2111	U
29	A	2112	G
29	A	2116	G
29	A	2117	A
29	A	2118	U
29	A	2119	A
29	A	2122	U
29	A	2126	A
29	A	2128	G
29	A	2132	U
29	A	2133	G
29	A	2136	G

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Mol	Chain	Res	Type
29	A	2147	A
29	A	2148	G
29	A	2157	G
29	A	2164	C
29	A	2165	C
29	A	2170	A
29	A	2171	A
29	A	2172	U
29	A	2173	A
29	A	2178	C
29	A	2198	A
29	A	2199	A
29	A	2204	G
29	A	2211	A
29	A	2225	A
29	A	2226	C
29	A	2238	G
29	A	2239	G
29	A	2283	C
29	A	2287	A
29	A	2288	A
29	A	2297	A
29	A	2305	U
29	A	2308	G
29	A	2311	A
29	A	2325	G
29	A	2327	A
29	A	2333	A
29	A	2335	A
29	A	2336	A
29	A	2343	U
29	A	2344	U
29	A	2350	C
29	A	2361	G
29	A	2383	G
29	A	2385	C
29	A	2402	U
29	A	2406	A
29	A	2425	A
29	A	2426	A
29	A	2428	G
29	A	2429	G

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Mol	Chain	Res	Type
29	A	2430	A
29	A	2435	A
29	A	2441	U
29	A	2447	G
29	A	2448	A
29	A	2475	C
29	A	2476	A
29	A	2478	A
29	A	2491	U
29	A	2494	G
29	A	2498	C
29	A	2502	G
29	A	2504	U
29	A	2505	G
29	A	2506	U
29	A	2513	A
29	A	2518	A
29	A	2520	C
29	A	2525	G
29	A	2529	G
29	A	2531	A
29	A	2554	U
29	A	2564	A
29	A	2566	A
29	A	2567	G
29	A	2572	A
29	A	2602	A
29	A	2609	U
29	A	2613	U
29	A	2615	U
29	A	2629	U
29	A	2639	A
29	A	2646	C
29	A	2647	U
29	A	2661	G
29	A	2662	A
29	A	2685	G
29	A	2689	U
29	A	2690	U
29	A	2714	G
29	A	2718	G
29	A	2726	A

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Mol	Chain	Res	Type
29	A	2729	G
29	A	2733	A
29	A	2744	G
29	A	2748	A
29	A	2757	A
29	A	2765	A
29	A	2778	A
29	A	2791	G
29	A	2798	U
29	A	2801	G
29	A	2818	U
29	A	2820	A
29	A	2835	A
29	A	2850	A
29	A	2867	G
29	A	2872	A
29	A	2873	A
29	A	2880	C
29	A	2884	U
29	A	2886	A
30	B	15	A
30	B	35	C
30	B	36	C
30	B	41	G
30	B	44	G
30	B	89	U
30	B	90	C
30	B	99	A
30	B	109	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A	271	G
29	A	404	A
29	A	1057	A
29	A	1328	A
29	A	1378	A
29	A	2127	G
29	A	2425	A
29	A	2505	G
29	A	2756	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
35	GNP	9	402	34	34,34,34	1.32	5 (14%)	47,54,54	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	GNP	9	402	34	-	2/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	9	402	GNP	PB-O3A	4.59	1.64	1.59
35	9	402	GNP	PB-O1B	3.25	1.51	1.46
35	9	402	GNP	PG-N3B	3.04	1.71	1.63
35	9	402	GNP	PG-O1G	2.84	1.50	1.46
35	9	402	GNP	PB-O2B	-2.27	1.50	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

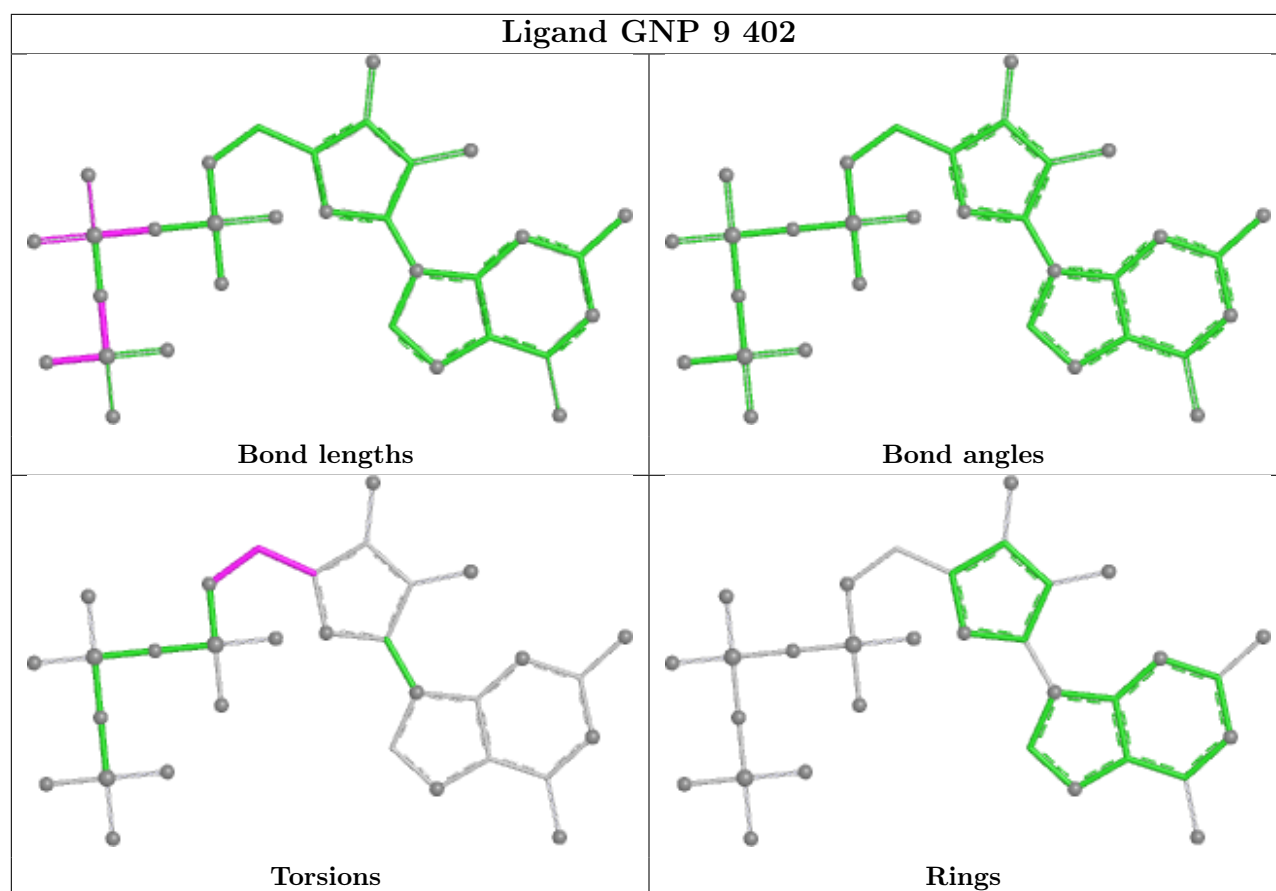
Mol	Chain	Res	Type	Atoms
35	9	402	GNP	C4'-C5'-O5'-PA
35	9	402	GNP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	9	402	GNP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

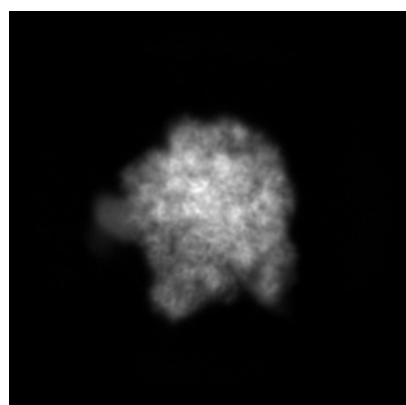
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12219. These allow visual inspection of the internal detail of the map and identification of artifacts.

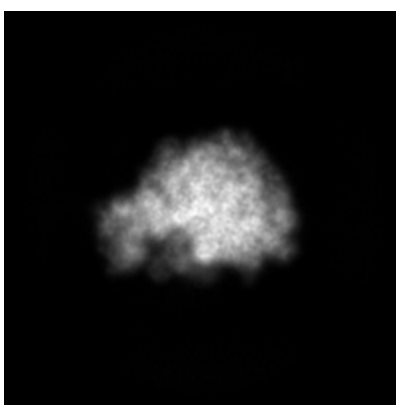
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

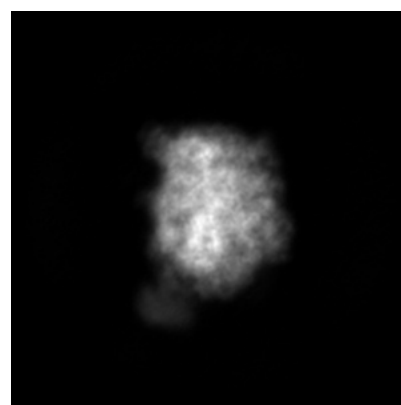
6.1.1 Primary map



X



Y

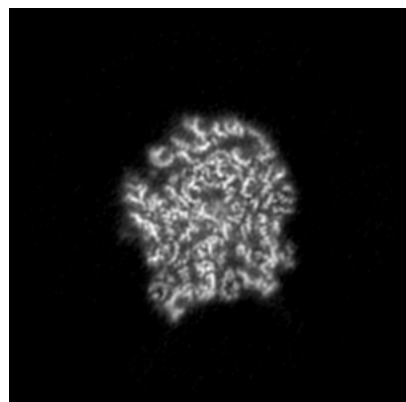


Z

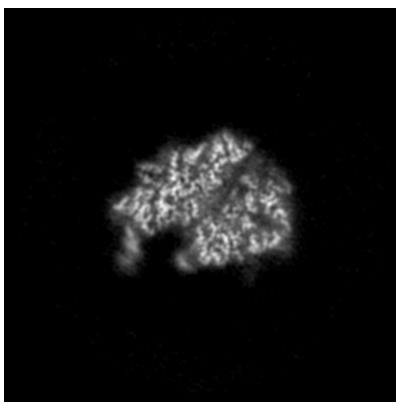
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

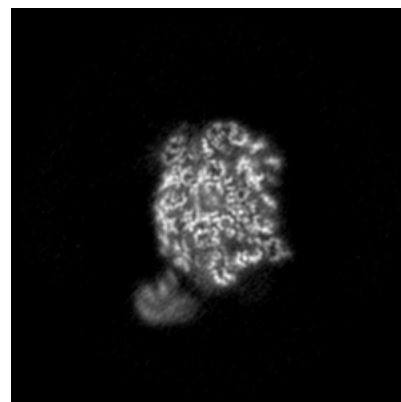
6.2.1 Primary map



X Index: 120



Y Index: 120

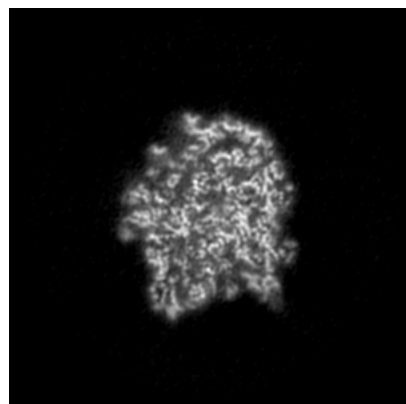


Z Index: 120

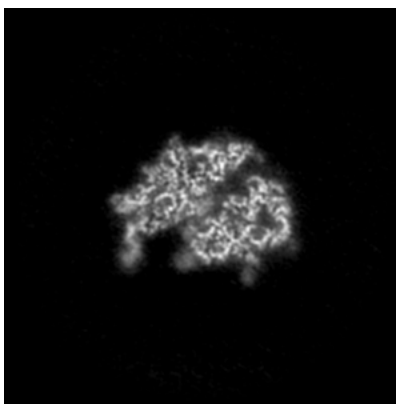
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

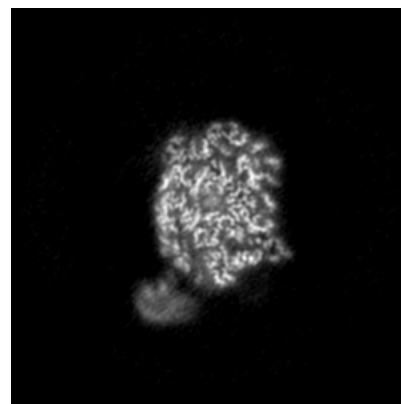
6.3.1 Primary map



X Index: 117



Y Index: 123

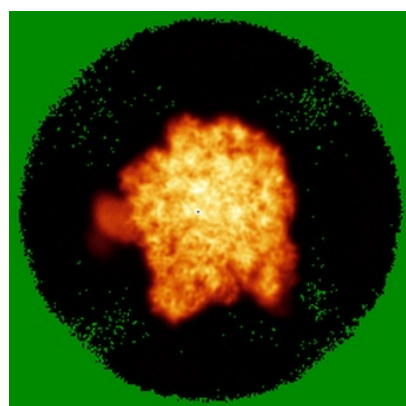


Z Index: 119

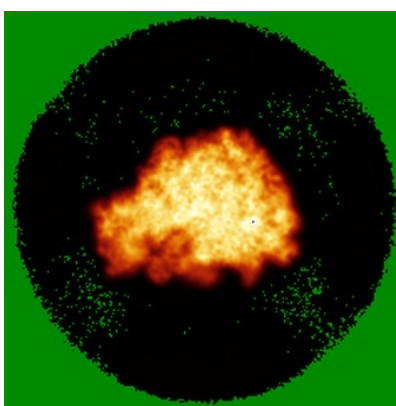
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

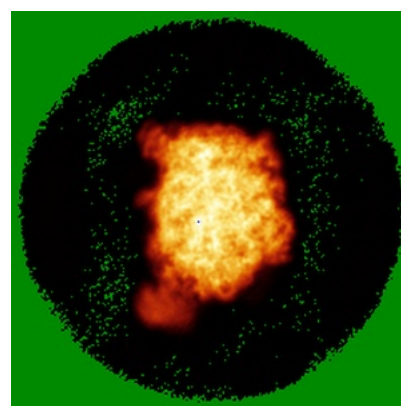
6.4.1 Primary map



X



Y

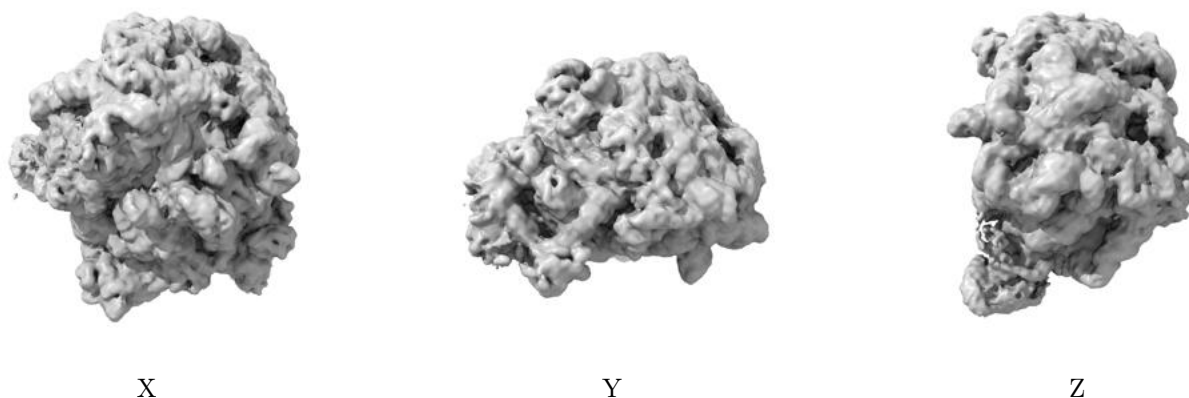


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

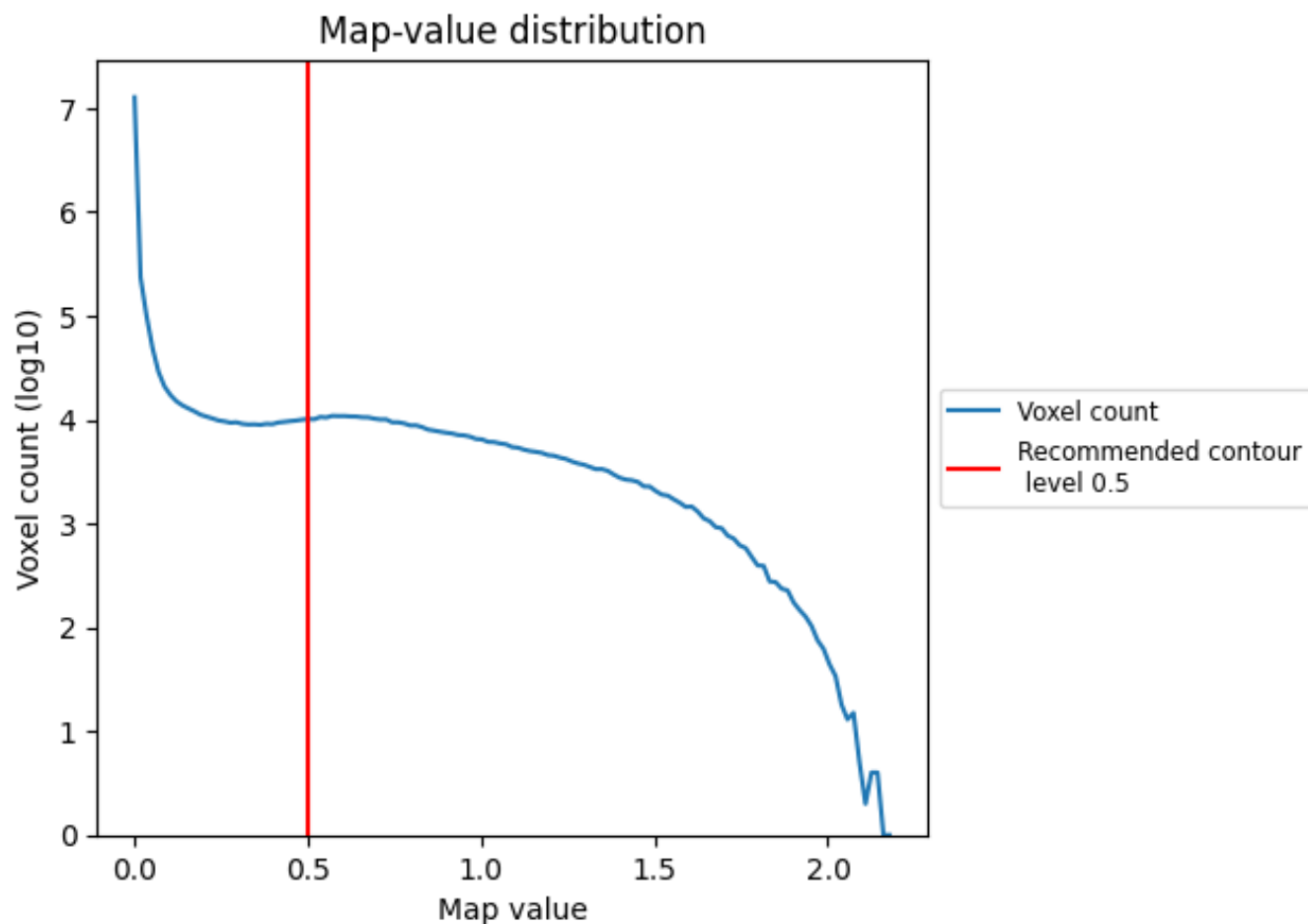
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

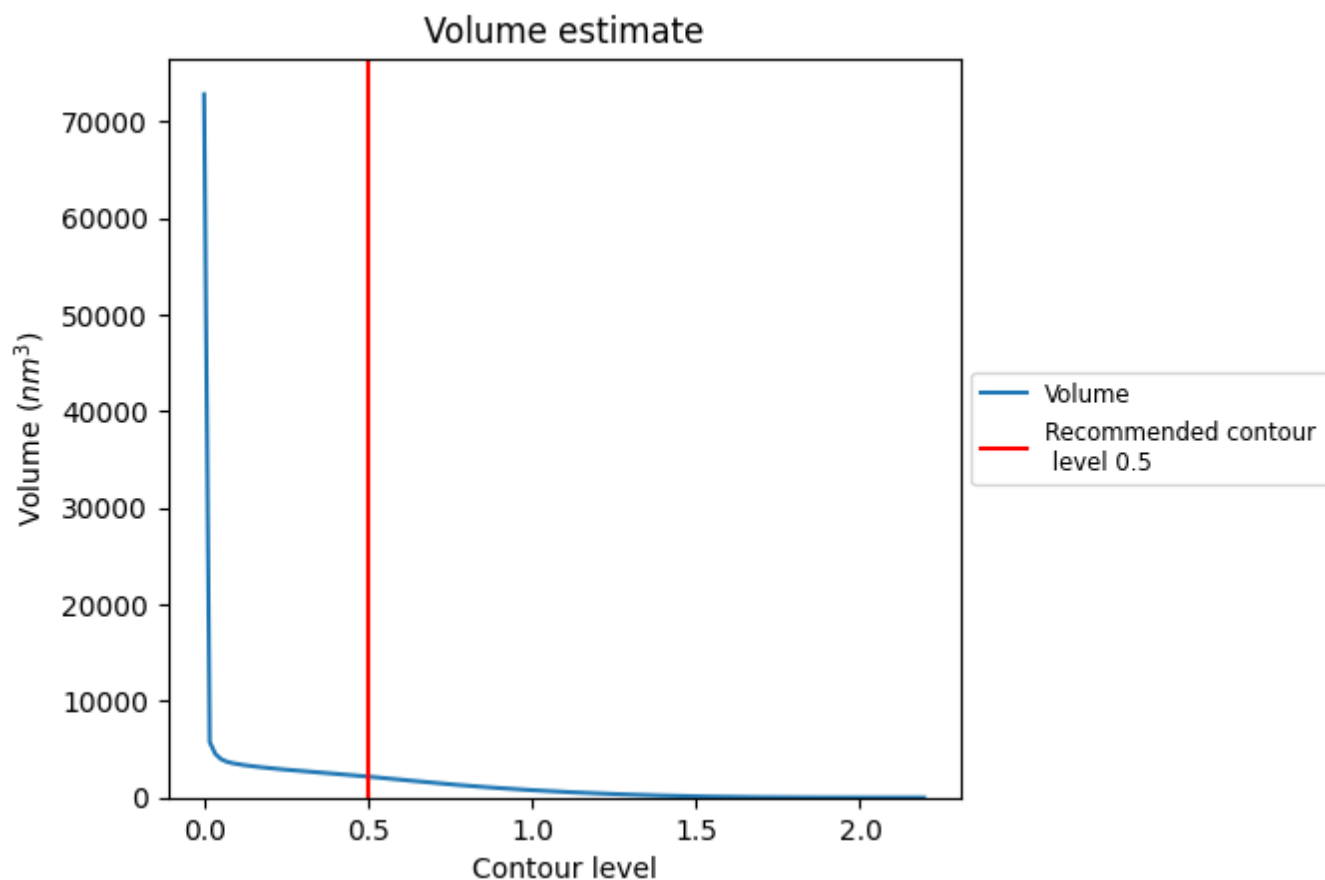
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

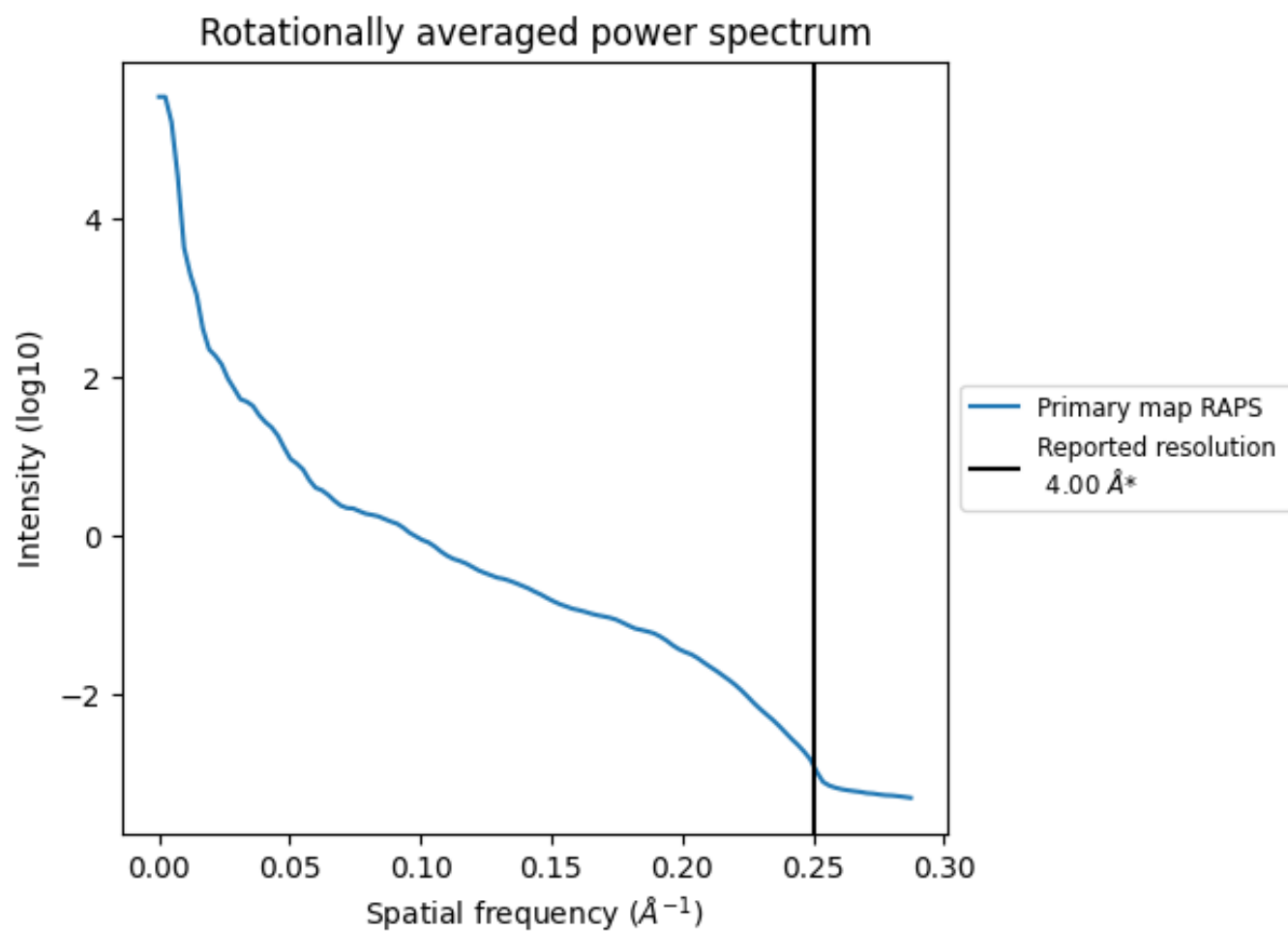
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2171 nm³; this corresponds to an approximate mass of 1962 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

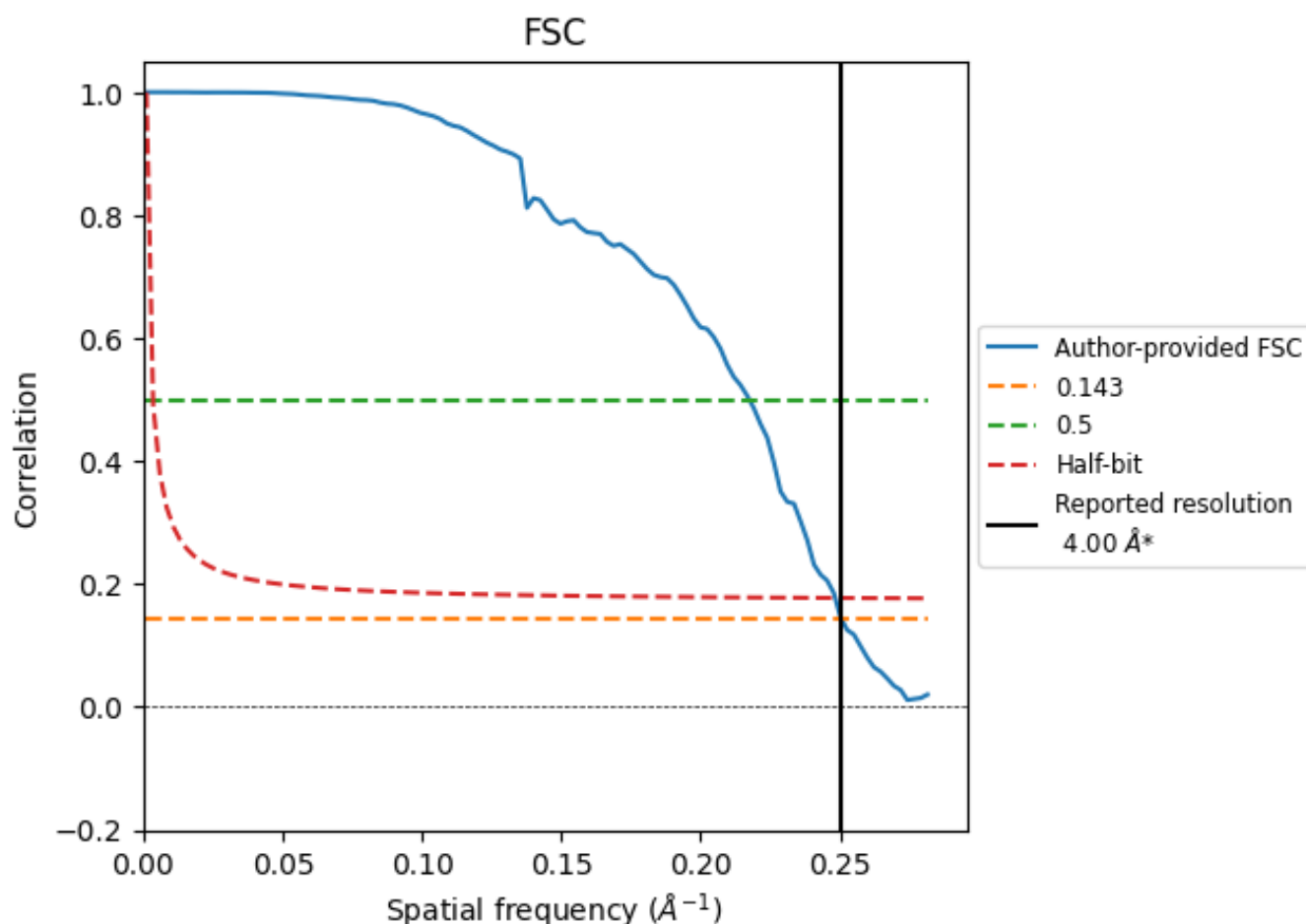


*Reported resolution corresponds to spatial frequency of 0.250 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

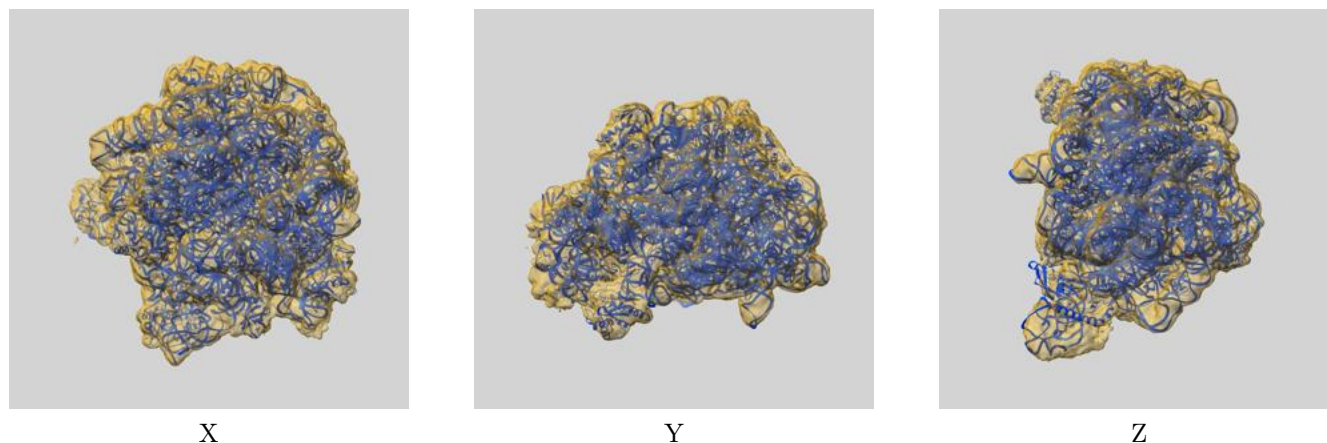
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.99	4.60	4.03
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

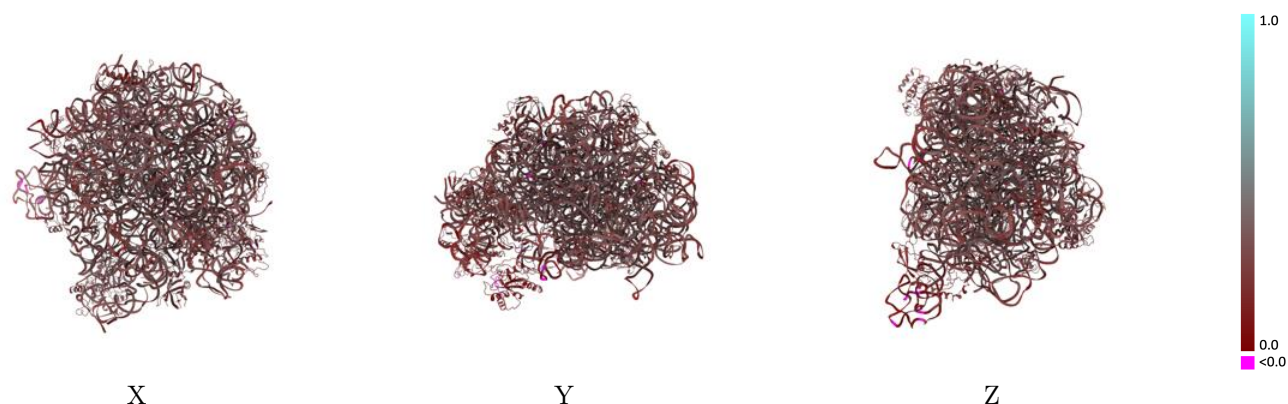
This section contains information regarding the fit between EMDB map EMD-12219 and PDB model 7BL6. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



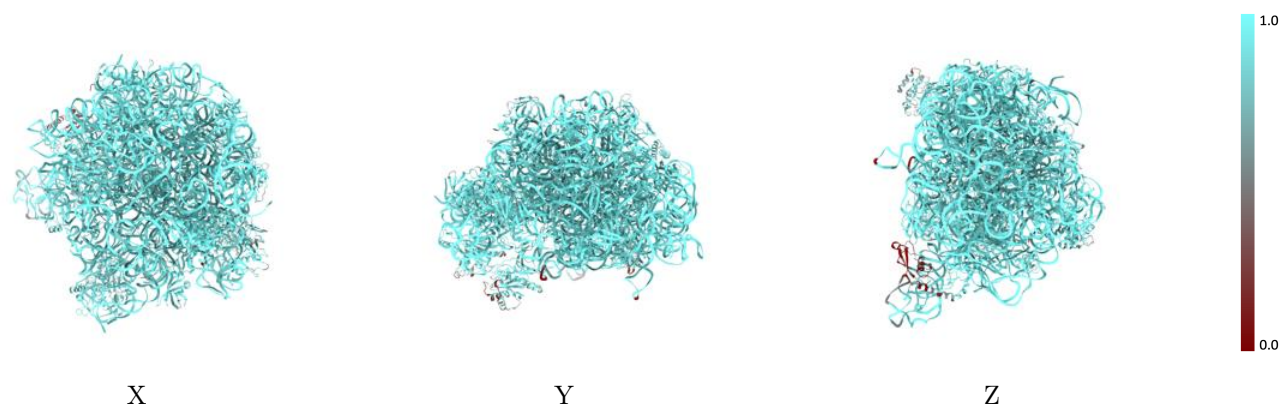
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



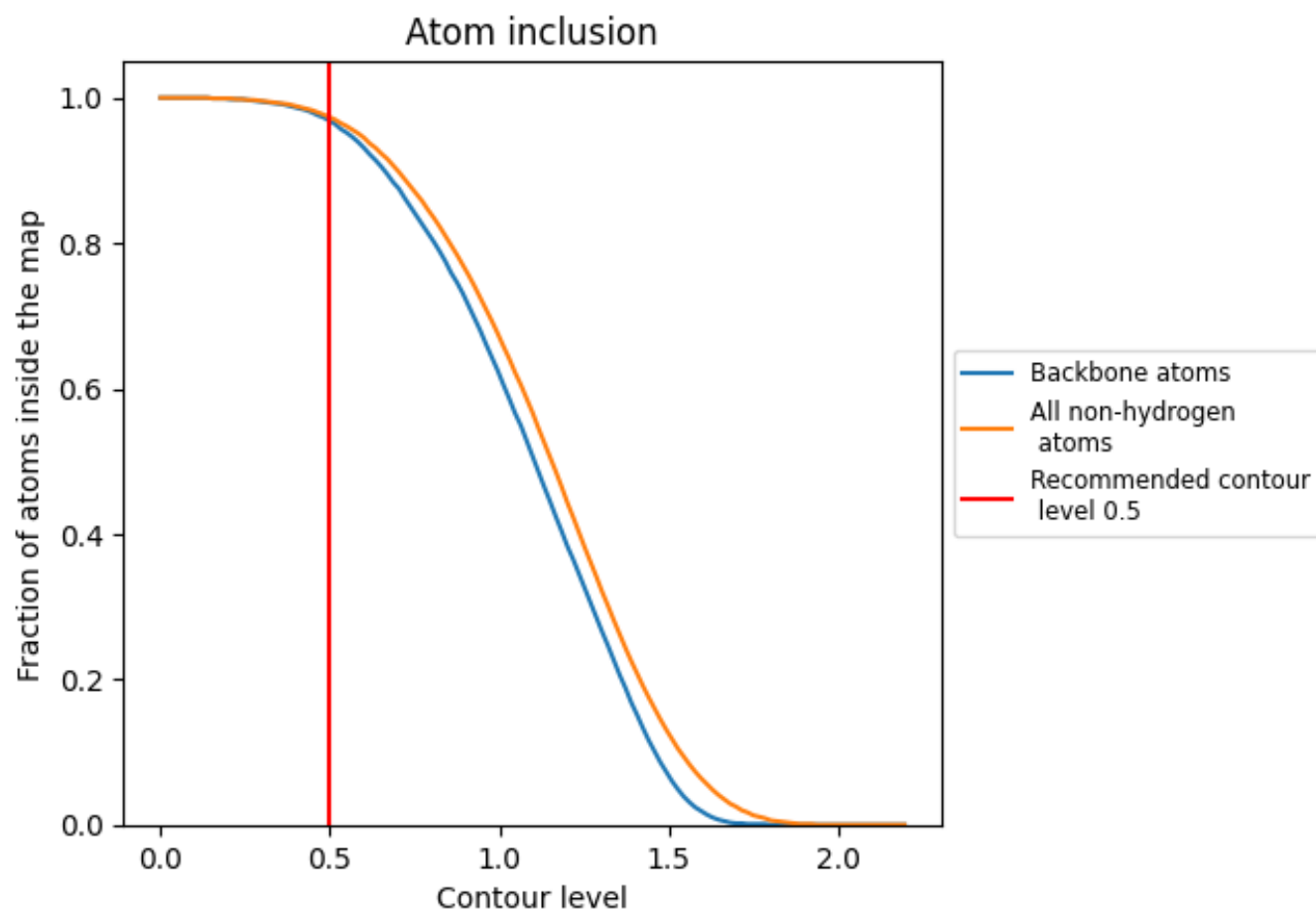
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.2890
0	 0.9810	 0.2670
1	 0.9950	 0.2680
2	 0.9970	 0.2870
3	 1.0000	 0.2860
9	 0.8530	 0.1990
A	 0.9900	 0.3010
B	 0.9970	 0.2850
C	 0.9910	 0.3020
D	 0.9700	 0.3000
E	 0.9160	 0.2710
F	 0.8990	 0.2090
G	 0.9000	 0.2490
H	 0.5700	 0.2020
J	 0.9850	 0.2910
K	 0.9770	 0.2810
L	 0.9560	 0.2820
M	 0.9810	 0.2930
N	 0.9920	 0.2700
O	 0.9710	 0.2530
P	 0.9600	 0.2810
Q	 0.9850	 0.2690
R	 0.9270	 0.2820
S	 0.9820	 0.2780
T	 0.9830	 0.2920
U	 0.9620	 0.2600
V	 0.9510	 0.2710
W	 0.9930	 0.2860
X	 0.9900	 0.2870
Y	 0.9500	 0.2140
Z	 0.9410	 0.2580
d	 0.6740	 0.1790
g	 0.9930	 0.2860

